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(54) **NL3 TIE receptor tyrosine kinase ligand homologues**

NL3 TIE Rezeptortyrosinekinase Ligandhomologe

Homologue NL3 du ligand du récepteur de kinase TIE

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Description**Field of the Invention**

5 **[0001]** The present invention concerns isolated nucleic acid molecules encoding novel TIE ligand homologues, the TIE ligand homologue proteins encoded by such nucleic acid molecules, as well as methods and means for making and using such nucleic acid and protein molecules, and antibodies binding the disclosed TIE ligand homologues.

Background Art

10 **[0002]** The abbreviations "TIE" or "tie" are acronyms, which stand for "tyrosine kinase containing 1g and EGF homology domains" and were coined to designate a new family of receptor tyrosine kinases which are almost exclusively expressed in vascular endothelial cells and early hemopoietic cells, and are characterized by the presence of an EGF-like domain, and extracellular folding units stabilized by intra-chain disulfide bonds, generally referred to as "immunoglobulin (1G)-like" folds. A tyrosine kinase homologous cDNA fragment from human leukemia cells (tie) was described by Partanen et al.,
 15 Proc. Natl. Acad. Sci. USA **87**, 8913-8917 (1990). The mRNA of this human "tie" receptor has been detected in all human fetal and mouse embryonic tissues, and has been reported to be localized in the cardiac and vascular endothelial cells. Korhonen et al., Blood **80**, 2548-2555 (1992); PCT Application Publication No. WO 93/14124 (published 22 July 1993). The rat homolog of human tie, referred to as "tie-1", was identified by Maisonpierre et al., Oncogene **8**, 1631-1637
 20 (1993). Another tie receptor, designated "tie-2" was originally identified in rats (Dumont et al., Oncogene **8**, 1293-1301 (1993)), while the human homolog of tie-2, referred to as "ork" was described in U.S. Patent No. 5,447,860 (Ziegler). The murine homolog of tie-2 was originally termed "tek." The cloning of a mouse tie-2 receptor from a brain capillary cDNA library is disclosed in PCT Application Publication No. WO 95/13387 (published 18 May 1995). The TIE receptors are believed to be actively involved in angiogenesis, and may play role in hemopoiesis as well.

25 **[0003]** The expression cloning of human TIE-2 ligands has been described in PCT Application Publication No. WO 96/1 1269 (published 18 April 1996) and in U.S. Patent No. 5,521,073 (published 28 May 1996). A vector designated as λ gt 10 encoding a TIE-2 ligand named "htie-2 ligand 1" or "hTL1" has been deposited under ATCC Accession No. 75928. A plasmid encoding another TIE-2 ligand designated "htie-2 2" or "hTL2" is available under ATCC Accession No. 75928. This second ligand has been described as an antagonist of the TAI-2 receptor. The identification of secreted
 30 human and mouse ligands for the TIE-2 receptor has been reported by Davis et al., Cell **87**, 1161-1169 (1996). The human ligand designated "Angiopoietin-1", to reflect its role in angiogenesis and potential action during hemopoiesis, is the same ligand as the ligand variously designated as "htie-2 1" or "hTL-1" in WO 96/11269. Angiopoietin-1 has been described to play an angiogenic role later and distinct from that of VEGF (Suri et al., Cell **87**, 1171-1180(1996)). Since TIE-2 is apparently upregulated during the pathologic angiogenesis requisite for tumor growth (Kaipainen et al., Cancer Res. **54**, 6571-6577 (1994)) angiopoietin-1 has been suggested to be additionally useful for specifically targeting tumor vasculature (Davis et al., supra).

Summary of the Invention

40 **[0004]** The present invention concerns novel human TIE ligand homologues with powerful effects on vasculature. The invention also provides for isolated nucleic acid molecules encoding such ligand homologues and vectors containing such nucleic acid molecules. The invention further concerns host cells transformed with such nucleic acid to produce the novel TIE ligand homologues. The novel ligand homologues may be agonists or antagonists of TIE receptors, known or hereinafter discovered. Their therapeutic or diagnostic use, including the delivery of other therapeutic or diagnostic
 45 agents to cells expressing the respective TIE receptors, is also within the scope of the present invention.

[0005] The present invention further provides antibodies specifically binding the TIE ligand homologues herein, and the use of such antibodies, for use in a medical treatment.

[0006] In another aspect, the invention concerns compositions comprising the novel ligand homologues or antibodies specifically binding it.

50 **[0007]** In a further aspect, the invention concerns conjugates of the novel TIE ligand homologues of the present invention with other therapeutic or cytotoxic agents, and compositions comprising such conjugates. The TIE-2 receptor has been reported to be upregulated during the pathologic angiogenesis that is requisite for tumor growth, and other TIE receptors might have similar properties. Accordingly, the conjugates of the TIE ligand homologues of the present invention to cytotoxic or other anti-tumor agents may be useful in specifically targeting tumor vasculature.

55 **[0008]** A method for identifying a cell that expresses a TIE receptor may comprise contacting a cell with a detectably labeled TIE ligand homologue of the present invention under conditions permitting the binding of such TIE ligand homologue to the TIE receptor, and determining whether such binding has indeed occurred.

[0009] A method for measuring the amount of a TIE ligand homologue of the present invention in a biological sample

may comprise contacting the biological sample with at least one antibody specifically binding the TIE ligand homologue and measuring the amount of the TIE ligand homologue-antibody complex formed.

[0010] A screening method for identifying polypeptide or small molecule agonists or antagonists of a TIE receptor may be based upon their ability to compete with a native or variant TIE ligand homologue of the present invention for binding to a corresponding TIE receptor.

[0011] In another aspect, the invention concerns use of a TIE ligand homologue of the present invention in the preparation of a medicament for inhibiting tumor growth.

[0012] Apoptosis of endothelial cells may be induced by administering an effective amount of a TIE ligand homologue of the present invention.

[0013] The TIE ligand homologues of the present invention may be administered alone, or in combination with each other and/or with other therapeutic or diagnostic agents, including members of the VEGF family. Combination therapies may lead to new approaches for treatment of conditions associated with unwanted endothelial cell growth, e.g. tumor treatment.

Brief Description of the Figures

[0014]

Figure 1 is a graphic depiction of the relationship of the ligand homologues NL2, NL3 and FLS 139 with the two known ligand homologues of the TIE2 receptor (h-TIE2L 1 and h-TIE2L2) and with other TIE ligand homologues disclosed in application Serial No. 08/933,821, filed on September 19, 1997.

Figure 2 is the nucleotide sequence of the TIE ligand NL2 (SEQ. ID. NO: 1) (DNA 22780).

Figure 3 is the amino acid sequence of the TIE ligand NL2 (SEQ. ID. NO:2).

Figure 4 is the nucleotide sequence of the TIE ligand NL3 (SEQ. ID. NO: 3) (DNA 33457).

Figure 5 is the amino acid sequence of the TIE ligand NL3 (SEQ. ID. NO: 4).

Figure 6 is the nucleotide sequence of the TIE ligand FLS139 (SEQ. ID NO 5) (DNA 16451).

Figure 7 is the amino acid sequence of the TIE ligand FLS139 (SEQ. 10 NO:6).

Figure 9 Northern blot showing the expression of the mRNAs of TIE ligand homologues NL3 in various tissues.

Detailed Description of the Invention

A. TIE LIGAND HOMOLOGUES AND NUCLEIC ACID MOLECULES ENCODING THEM

[0015] The TIE ligand homologues of the present invention include the native human ligand homologue designated NL3 (SEQ. ID. NO: 4) and its homologs in other, non-human mammalian species, including, but not limited to, higher mammals, such as monkey; rodents, such as mice, rats, hamster; porcine; equine; bovine; naturally occurring allelic and splice variants.

[0016] The amino acid sequence of native NL3, as disclosed herein, is about 30% identical with that of hTL-1 and about 29% identical with that of hTL-2. The native TIE ligand homologues of the present invention are substantially free of other proteins with which they are associated in their native environment. This definition is not limited in any way by the method(s) by which the TIE ligand homologues of the present invention are obtained, and includes all ligand homologues otherwise within the definition, whether purified from natural source, obtained by recombinant DNA technology, synthesized, or prepared by any combination of these and/or other techniques. The amino acid sequence variants of the native TIE ligand homologues of the present invention shall have at least 90%, preferably, at least 95%, more preferably at least 98%, most preferably at least 99% sequence identity with a full-length, native human TIE ligand homologue of the present invention, or with the fibrinogen-like domain of a native human TIE ligand homologue of the present invention. Such amino acid sequence variants preferably exhibit or inhibit a qualitative biological activity of a native TIE ligand homologue.

[0017] The term "fibrinogen domain" or "fibrinogen-like domain" is used to refer to amino acids from about position 278 to about position 498 in the known hTL-1 amino acid sequence; amino acids from about position 276 to about position 496 in the known hTL-2 amino acid sequence; amino acids from about position 77 to about position 288 in the amino acid sequence of NL3; and to homologous domains in other TIE ligand homologues. The NL3 fibrinogen-like domain is about 37% identical to the fibrinogen-like domains of hTL-1 and hTL-2.

[0018] The term "nucleic acid molecule" includes RNA, DNA and cDNA molecules. It will be understood that, as a result of the degeneracy of the genetic code, a multitude of nucleotide sequences encoding a given TIE ligand may be produced. The present invention specifically contemplates every possible variation of nucleotide sequences, encoding the TIE ligand homologues of the present invention, based upon all possible codon choices. Although nucleic acid molecules which encode the TIE ligand homologues herein are preferably capable of hybridizing, under stringent con-

ditions, to a naturally occurring TIE ligand homologue gene, it may be advantageous to produce nucleotide sequences encoding TIE ligand homologues, which possess a substantially different codon usage. For example, codons may be selected to increase the rate at which expression of the polypeptide occurs in a particular prokaryotic or eukaryotic host cells, in accordance with the frequency with which a particular codon is utilized by the host. In addition, RNA transcripts with improved properties, e.g. half-life can be produced by proper choice of the nucleotide sequences encoding a given TIE ligand homologue.

[0019] "Sequence identity" shall be determined by aligning the two sequences to be compared following the Clustal method of multiple sequence alignment (Higgins et al., Comput. Appl. Biosci. 5, 151-153(1989), and Higgins et al., Gene 73, 237-244 (1988)) that is incorporated in version 1.6 of the Lasergene biocomputing software (DNASTAR, Inc., Madison, Wisconsin), or any updated version or equivalent of this software.

[0020] "Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

[0021] "Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42 °C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1 % sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

[0022] "Moderately stringent conditions" may be identified as described by Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0023] The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a TIE ligand homologue polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

[0024] The terms "biological activity" and "biologically active" with regard to a TIE ligand homologue of the present invention refer to the ability of a molecule to specifically bind to and signal through a native receptor of a TIE ligand, known or hereinafter discovered, (hereinafter referred to as a "TIE receptor"), e. g. a native TIE-2 receptor, or to block the ability of native TIE receptor (eg. TIE-2) to participate in signal transduction. Thus, the (native and variant) TIE ligands of the present invention include agonists and antagonists of a native TIE, e.g. TIE-2, receptor. Preferred biological activities of the TIE ligands of the present invention include the ability to induce or inhibit vascularization. The ability to induce vascularization will be useful for the treatment of biological conditions and diseases, where vascularization is desirable, such as wound healing, ischaemia, and diabetes. On the other hand, the ability to inhibit or block vascularization may, for example, be useful in preventing or attenuating tumor growth. Another preferred biological activity is the ability to affect muscle growth or development. A further preferred biological activity is the ability to influence bone development, maturation, or growth. Yet another preferred biological activity is the ability to inhibit endothelial cell growth and/or induce apoptosis.

[0025] The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (e.g. ^{131}I , ^{125}I , ^{90}Y and Re^{186}), chemotherapeutic agents, and toxins such as enzymatically active toxins of bacterial, fungal, plant or animal origin, or fragments thereof.

[0026] A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include adriamycin, doxorubicin, epirubicin, 5-fluorouracil, cytosine arabinoside ("Ara-C"), cyclophosphamide, thiopeta, busulfan, cytosine, taxoids, e.g. paclitaxel (Taxol, Bristol-Myers Squibb Oncology, Princeton, NJ), and doxetaxel (Taxotere, Rhône-Poulenc Rorer, Antony, France), taxotere, methotrexate, cisplatin, melphalan, vinblastine, bleomycin, etoposide, ifosfamide, mitomycin C, mitoxantrone, vincristine, vinorelbine, carboplatin, teniposide, daunomycin, carminomycin, aminopterin, dactinomycin, mitomycins, esperamicins (see U.S. Pat. No. 4,675,187), melphalan and other related nitrogen mustards. Also included in this definition are hormonal agents that act to regulate or inhibit hormone action on tumors such as tamoxifen and onapristone.

[0027] A "growth inhibitory agent" when used herein refers to a compound or composition which inhibits growth of a cell, especially cancer cell overexpressing any of the genes identified herein, either *in vitro* or *in vivo*. Thus, the growth inhibitory agent is one which significantly reduces the percentage of cells overexpressing such genes in S phase. Examples of growth inhibitory agents include agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxol, and topo II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in *The Molecular Basis of Cancer*, Mendelsohn and Israel, eds., Chapter I, entitled "Cell cycle regulation, oncogens, and antineoplastic drugs" by Murakami *et al.* (WB Saunders: Philadelphia, 1995), especially p: 13.

[0028] "Doxorubicin" is an anthracycline antibiotics. The full chemical name of doxorubicin is (8S-cis)-10-[(3-amino-2,3,6-trideoxy- α -L-lyxo-hexapyranosyl)oxy]-7,8,9,10-tetrahydro-6,8,10-trihydroxy-8-(hydroxyacetyl)-1-methoxy-5,12-naphthacenedione.

[0029] The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; Fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor- α and - β ; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF- β ; platelet-growth factor; transforming growth factors (TGFs) such as TGF- α and TGF- β ; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon- α , - β , and - γ ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1 α , IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-11, IL-12; a tumor necrosis factor such as TNF- α or TNF- β ; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

[0030] "Vascular endothelial growth factor"/"vascular permeability factor" (VEGF/VPF) is an endothelial cell-specific mitogen which has recently been shown to be stimulated by hypoxia and required for tumor angiogenesis (Senger *et al.*, *Cancer* 46: 5629-5632 (1986); Kim *et al.*, *Nature* 362: 841-844 (1993); Schweiki *et al.*, *Nature* 359: 843-845 (1992); Plate *et al.*, *Nature* 359: 845-848 (1992)). It is a 34-43 kDa (with the predominant species at about 45 kDa) dimeric, disulfide-linked glycoprotein synthesized and secreted by a variety of tumor and normal cells. In addition, cultured human retinal cells such as pigment epithelial cells and pericytes have been demonstrated to secrete VEGF and to increase VEGF gene expression in response to hypoxia (Adamis *et al.*, *Biochem. Biophys. Res. Commun.* 193: 631-638 (1993); Plouet *et al.*, *Invest. Ophthalmol. Vis. Sci.* 14: 900 (1992); Adamis *et al.*, *Invest. Ophthalmol. Vis. Sci.* 34: 1440 (1993); Aiello *et al.*, *Invest. Ophthalmol. Vis. Sci.* 35: 1868 (1994); Simorre-pinatel *et al.*, *Invest. Ophthalmol. Vis. Sci.* 25: 3393-3400 (1994)). In contrast, VEGF in normal tissues is relatively low. Thus, VEGF appears to play a principle role in many pathological states and processes related to neovascularization. Regulation of VEGF expression in tissues affected by the various conditions described above could therefore be key in treatment or preventative therapies associated with hypoxia.

[0031] The term "agonist" is used to refer to peptide and non-peptide analogs of the native TIE ligand homologues of the present invention provided that they have the ability to signal through a native TIE receptor (e.g. TIE-2). In other words, the term "agonist" is defined in the context of the biological role of the TIE receptor, and not in relation to the biological role of a native TIE ligand homologue, which, as noted before, may be an agonist or antagonist of the TIE receptor biological function. Preferred agonists possess the preferred biological activities of the TIE homologues as listed above, and include promoters of vascularization, molecules that play a role in bone formation maturation or growth, and promoters of muscle growth and/or development.

[0032] The term "antagonist" is used to refer to peptide and non-peptide analogs of the native TIE ligand homologues of the present invention and to antibodies specifically binding such native TIE ligand homologues, provided that they have the ability to inhibit the biological function of a native TIE receptor (e.g. TIE-2). Again, the term "antagonist" is

defined in the context of the biological role of the TIE receptor, and not in relation to the biological activity of a native TIE ligand homologue, which may be either an agonist or an antagonist of the TIE receptor biological function. Preferred antagonists are inhibitors of vasculogenesis, or pathological bone or muscle development or growth

[0033] "Tumor", as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues.

[0034] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include breast cancer, prostate cancer, colon cancer, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, colorectal cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, vulval cancer, thyroid cancer, hepatic carcinoma and various types of head and neck cancer.

[0035] "Treatment" is an intervention performed with the intention of preventing the development or altering the pathology of a disorder. Accordingly, "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented. In tumor (e.g. cancer) treatment, a therapeutic agent may directly decrease the pathology of tumor cells, or render the tumor cells more susceptible to treatment by other therapeutic agents, e.g. radiation and/or chemotherapy.

[0036] The "pathology" of cancer includes all phenomena that compromise the well-being of the patient. This includes, without limitation, abnormal or uncontrollable cell growth, metastasis, interference with the normal functioning of neighboring cells, release of cytokines or other secretory products at abnormal levels, suppression or aggravation of inflammatory or immunological response, etc.

[0037] "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, horses, cats, cows, etc. Preferably, the mammal is human.

[0038] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0039] The term "functional derivative" is used to define biologically active amino acid sequence variants of the native TIE ligand homologues of the present invention, as well as covalent modifications, including derivatives obtained by reaction with organic derivatizing agents, post-translational modifications; derivatives with nonproteinaceous polymers, and immunoadhesins.

[0040] The term "isolated" when used to describe the various polypeptides described herein, means polypeptides that have been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the TIE ligand's natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0041] An "isolated" nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the nucleic acid. An isolated nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from the nucleic acid molecule as it exists in natural cells. However, an isolated nucleic acid molecule includes nucleic acid molecules contained in cells that ordinarily express an TIE ligand of the present invention, where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

[0042] The term "amino acid sequence variant" refers to molecules with some differences in their amino acid sequences as compared to a native amino acid sequence.

[0043] Substitutional variants are those that have at least one amino acid residue in a native sequence removed and a different amino acid inserted in its place at the same position. The substitutions may be single, where only one amino acid in the molecule has been substituted, or they may be multiple, where two or more amino acids have been substituted in the same molecule.

[0044] Insertional variants are those with one or more amino acids inserted immediately adjacent to an amino acid at a particular position in a native sequence. Immediately adjacent to an amino acid means connected to either the α -carboxy or α -amino functional group of the amino acid.

[0045] Deletional variants are those with one or more amino acids in the native amino acid sequence removed. Ordinarily, deletional variants will have one or two amino acids deleted in a particular region of the molecule. Deletional variants include those having C- and/or N-terminal deletions (truncations) as well as variants with internal deletions of

one or more amino acids. The preferred deletional variants of the present invention contain deletions outside the fibrinogen-like domain of a native TIE ligand homologue of the present invention.

[0046] The amino acid sequence variants may contain various combinations of amino acid substitutions, insertions and/or deletions, to produce molecules with optimal characteristics.

[0047] The amino acids may be classified according to the chemical composition and properties of their side chains. They are broadly classified into two groups, charged and uncharged. Each of these groups is divided into subgroups to classify the amino acids more accurately.

I. Charged Amino Acids

[0048] Acidic Residues: aspartic acid, glutamic acid

[0049] Basic Residues: lysine, arginine, histidine

II. Uncharged Amino Acids

[0050] Hydrophilic Residues: serine, threonine, asparagine, glutamine

[0051] Aliphatic Residues: glycine, alanine, valine, leucine, isoleucine

[0052] Non-polar Residues: cysteine, methionine, proline

[0053] Aromatic Residues: phenylalanine, tyrosine, tryptophan

[0054] Conservative substitutions involve exchanging a member within one group for another member within the same group, whereas non-conservative substitutions will entail exchanging a member of one of these classes for another. Variants obtained by non-conservative substitutions are expected to result in significant changes in the biological properties/function of the obtained variant

[0055] Amino acid sequence deletions generally range from about 1 to 30 residues, more preferably about 1 to 10 residues, and typically are contiguous. Deletions may be introduced into regions not directly involved in the interaction with a native TIE receptor. Deletions are preferably performed outside the fibrinogen-like regions at the C-terminus of the TIE ligand homologues of the present invention.

[0056] Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions (i.e. insertions within the TIE ligand homologue amino acid sequence) may range generally from about 1 to 10 residues, more preferably 1 to 5 residues, more preferably 1 to 3 residues. Examples of terminal insertions include the TIE ligand homologues with an N-terminal methionyl residue, an artifact of its direct expression in bacterial recombinant cell culture, and fusion of a heterologous N-terminal signal sequence to the N-terminus of the TIE ligand homologue molecule to facilitate the secretion of the mature TIE ligand homologue from recombinant host cells. Such signal sequences will generally be obtained from, and thus homologous to, the intended host cell species. Suitable sequences include, for example, STII or Ipp for *E. coli*, alpha factor for yeast, and viral signals such as herpes gD for mammalian cells.

[0057] Other insertional variants of the native TIE ligand molecules include the fusion of the N- or C-terminus of the TIE ligand homologue molecule to immunogenic polypeptides, e.g. bacterial polypeptides such as beta-lactamase or an enzyme encoded by the *E. coli* trp locus, or yeast protein, and C-terminal fusions with proteins having a long half-life such as immunoglobulin regions (preferably immunoglobulin constant regions), albumin, or ferritin, as described in WO 89/02922 published on 6 April 1989.

[0058] Since it is often difficult to predict in advance the characteristics of a variant TIE ligand homologue, it will be appreciated that some screening will be needed to select the optimum variant.

[0059] Amino acid sequence variants of native TIE ligand homologues of the present invention are prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant TIE ligand homologue DNA, or by *in vitro* synthesis of the desired polypeptide. There are two principal variables in the construction of amino acid sequence variants: the location of the mutation site and the nature of the mutation. With the exception of naturally-occurring alleles, which do not require the manipulation of the DNA sequence encoding the TIE ligand homologue, the amino acid sequence variants of the TIE ligand homologues are preferably constructed by mutating the DNA. either to arrive at an allele or an amino acid sequence variant that does not occur in nature.

[0060] One group of the mutations will be created within the domain or domains of the TIE ligand homologues of the present invention identified as being involved in the interaction with a TIE receptor, e.g. TIE-1 or TIE-2, or a receptor yet to be discovered.

[0061] Alternatively or in addition, amino acid alterations can be made at sites that differ in TIE ligand homologues from various species, or in highly conserved regions, depending on the goal to be achieved.

[0062] Sites at such locations will typically be modified in series, e.g. by (1) substituting first with conservative choices and then with more radical selections depending upon the results achieved, (2) deleting the target residue or residues,

or (3) inserting residues of the same or different class adjacent to the located site, or combinations of options 1-3.

[0063] One helpful technique is called "alanine scanning" (Cunningham and Wells, Science **244**, 1081-1085 [1989]). Here, a residue or group of target residues is identified and substituted by alanine or polyalanine. Those domains demonstrating functional sensitivity to the alanine substitutions are then refined by introducing further or other substituents at or for the sites of alanine substitution.

[0064] After identifying the desired mutation(s), the gene encoding an amino acid sequence variant of a TIE ligand homologue can, for example, be obtained by chemical synthesis as hereinabove described.

[0065] More preferably, DNA encoding a TIE ligand homologue amino acid sequence variant is prepared by site-directed mutagenesis of DNA that encodes an earlier prepared variant or a nonvariant version of the ligand. Site-directed (site-specific) mutagenesis allows the production of ligand variants through the use of specific oligonucleotide sequences that encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 20 to 25 nucleotides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered. In general, the techniques of site-specific mutagenesis are well known in the art, as exemplified by publications such as, Edelman *et al.*, DNA **2**, 183 (1983). As will be appreciated, the site-specific mutagenesis technique typically employs a phage vector that exists in both a single-stranded and double-stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M 13 phage, for example, as disclosed by Messing *et al.*, Third Cleveland Symposium on Macromolecules and Recombinant DNA, A. Walton, ed., Elsevier, Amsterdam (1981). This and other phage vectors are commercially available and their use is well known to those skilled in the art. A versatile and efficient procedure for the construction of oligodeoxynucleotide directed site-specific mutations in DNA fragments using M 13-derived vectors was published by Zoller, M.J. and Smith, M., Nucleic Acids Res. **10**, 6487-6500 [1982]. Also, plasmid vectors that contain a single-stranded phage origin of replication (Veira *et al.*, Meth. Enzymol. **153**, 3 [1987]) may be employed to obtain single-stranded DNA. Alternatively, nucleotide substitutions are introduced by synthesizing the appropriate DNA fragment *in vitro*, and amplifying it by PCR procedures known in the art.

[0066] In general, site-specific mutagenesis herewith is performed by first obtaining a single-stranded vector that includes within its sequence a DNA sequence that encodes the relevant protein. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically, for example, by the method of Crea *et al.*, Proc. Natl. Acad. Sci. USA **75**, 5765 (1978). This primer is then annealed with the single-stranded protein sequence-containing vector, and subjected to DNA-polymerizing enzymes such as, *E. coli* polymerase I Klenow fragment, to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate host cells such as JP101 cells, and clones are selected that include recombinant vectors bearing the mutated sequence arrangement. Thereafter, the mutated region may be removed and placed in an appropriate expression vector for protein production.

[0067] The PCR technique may also be used in creating amino acid sequence variants of a TIE ligand. When small amounts of template DNA are used as starting material in a PCR, primers that differ slightly in sequence from the corresponding region in a template DNA can be used to generate relatively large quantities of a specific DNA fragment that differs from the template sequence only at the positions where the primers differ from the template. For introduction of a mutation into a plasmid DNA, one of the primers is designed to overlap the position of the mutation and to contain the mutation; the sequence of the other primer must be identical to a stretch of sequence of the opposite strand of the plasmid, but this sequence can be located anywhere along the plasmid DNA. It is preferred, however, that the sequence of the second primer is located within 200 nucleotides from that of the first, such that in the end the entire amplified region of DNA bounded by the primers can be easily sequenced. PCR amplification using a primer pair like the one just described results in a population of DNA fragments that differ at the position of the mutation specified by the primer, and possibly at other positions, as template copying is somewhat error-prone.

[0068] If the ratio of template to product material is extremely low, the vast majority of product DNA fragments incorporate the desired mutation(s). This product material is used to replace the corresponding region in the plasmid that served as PCR template using standard DNA technology. Mutations at separate positions can be introduced simultaneously by either using a mutant second primer or performing a second PCR with different mutant primers and ligating the two resulting PCR fragments simultaneously to the vector fragment in a three (or more) part ligation.

[0069] In a specific example of PCR mutagenesis, template plasmid DNA (1 μ g) is linearized by digestion with a restriction endonuclease that has a unique recognition site in the plasmid DNA outside of the region to be amplified. Of this material, 100 ng is added to a PCR mixture containing PCR buffer, which contains the four deoxynucleotide triphosphates and is included in the GeneAmp^R kits (obtained from Perkin-Elmer Cetus, Norwalk, CT and Emeryville, CA), and 25 pmole of each oligonucleotide primer, to a final volume of 50 μ l. The reaction mixture is overlaid with 35 μ l mineral oil. The reaction is denatured for 5 minutes at 100°C, placed briefly on ice, and then 1 μ l *Thermus aquaticus* (Tag) DNA polymerase (5 units/l), purchased from Perkin-Elmer Cetus, Norwalk, CT and Emeryville, CA) is added below the mineral

oil layer. The reaction mixture is then inserted into a DNA Thermal Cycler (purchased from Perkin-Elmer Cetus) programmed as follows:

2 min. 55°C

30 sec. 72°C. then 19 cycles of the following:

30 sec. 94°C,

30 sec. 55°C, and

30 sec. 72°C.

[0070] At the end of the program, the reaction vial is removed from the thermal cycler and the aqueous phase transferred to a new vial, extracted with phenol/chloroform(50:50 vol), and ethanol precipitated, and the DNA is recovered by standard procedures. This material is subsequently subjected to appropriate treatments for insertion into a vector.

[0071] Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells *et al.* (Gene 34, 315 (1985)). The starting material is the plasmid (or vector) comprising the TIE ligand homologue DNA to be mutated. The codon(s) within the TIE ligand homologue to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the DNA encoding the TIE ligand homologue. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction site but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are compatible with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated TIE ligand homologue DNA sequence.

[0072] Additionally, the so-called phagemid display method may be useful in making amino acid sequence variants of native or variant TIE ligand homologues. This method involves (a) constructing a replicable expression vector comprising a first gene encoding an receptor to be mutated, a second gene encoding at least a portion of a natural or wild-type phage coat protein wherein the first and second genes are heterologous, and a transcription regulatory element operably linked to the first and second genes, thereby forming a gene fusion encoding a fusion protein; (b) mutating the vector at one or more selected positions within the first gene thereby forming a family of related plasmids; (c) transforming suitable host cells with the plasmids; (d) infecting the transformed host cells with a helper phage having a gene encoding the phage coat protein; (e) culturing the transformed infected host cells under conditions suitable for forming recombinant phagemid particles containing at least a portion of the plasmid and capable of transforming the host, the conditions adjusted so that no more than a minor amount of phagemid particles display more than one copy of the fusion protein on the surface of the particle; (f) contacting the phagemid particles with a suitable antigen so that at least a portion of the phagemid particles bind to the antigen; and (g) separating the phagemid particles that bind from those that do not. Steps (d) through (g) can be repeated one or more times. Preferably in this method the plasmid is under tight control of the transcription regulatory element, and the culturing conditions are adjusted so that the amount or number of phagemid particles displaying more than one copy of the fusion protein on the surface of the particle is less than about 1%. Also, preferably, the amount of phagemid particles displaying more than one copy of the fusion protein is less than 10% of the amount of phagemid particles displaying a single copy of the fusion protein. Most preferably, the amount is less than 20%. Typically in this method, the expression vector will further contain a secretory signal sequence fused to the DNA encoding each subunit of the polypeptide and the transcription regulatory element will be a promoter system. Preferred promoter systems are selected from *lac* Z, λ_{PL} , *tac*, T7 polymerase, tryptophan, and alkaline phosphatase promoters and combinations thereof. Also, normally the method will employ a helper phage selected from M13K07, M13R408, M13-VCS, and Phi X 174. The preferred helper phage is M13K07, and the preferred coat protein is the M13 Phage gene III coat protein. The preferred host is *E. coli*, and protease-deficient strains of *E. coli*.

[0073] Further details of the foregoing and similar mutagenesis techniques are found in general textbooks, such as, for example, Sambrook *et al.*, *Molecular Cloning: A laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989), and *Current Protocols in Molecular Biology*, Ausubel *et al.*, eds., Wiley-Interscience, 1991.

[0074] "Immunoadhesins" are chimeras which are traditionally constructed from a receptor sequence linked to an appropriate immunoglobulin constant domain sequence (immunoadhesins). Such structures are well known in the art. Immunoadhesins reported in the literature include fusions of the T cell receptor* [Gascoigne *et al.*, *Proc. Natl.Acad. Sci. USA* 84, 2936-2940(1987)]; CD4* (Capon *et al.*, *Nature* 337, 525-531 (1989); Traunecker *et al.*, *Nature* 339, 68-70 (1989);

Zenmeissl *et al.*, *DNA Cell Biol. USA* 9, 347-353 (1990); Bym *et al.*, *Nature* 344, 667-670 (1990); L-selectin (homing receptor) [Watson *et al.*, *J. Cell. Biol.* 110, 2221-2229 (1990); Watson *et al.*, *Nature* 349, 164-167 (1991)]; CD44* [Aruffo *et al.*, *Cell* 61, 1303-1313 (1990)]; CD28* and B7* [Linsley *et al.*, *J. Exp. Med.* 173, 721-730 (1991)]; CTLA-4* [Lisley *et al.*, *J. Exp. Med.* 174, 561-569 (1991)]; CD22* [Stamenkovic *et al.*, *Cell* 66, 1133-1144 (1991)]; TNF receptor [Ashkenazi *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 10535-10539 (1991); Lesslauer *et al.*, *Eur. J. Immunol.* 27, 2883-2886 (1991); Peppel *et al.*, *J. Exp. Med.* 174, 1483-1489 (1991)]; NP receptors [Bennen *et al.*, *J. Biol. Chem.* 266, 23060-23067 (1991)]; 1gE receptor α -chain* [Ridgway and Gorman, *J. Cell-Biol.* 115, absir. 1448 (1991)]; HGF receptor [Mark, M.R. *et al.*, 1992, *J. Biol. Chem.*, submitted], where the asterisk (*) indicates that the receptor is member of the immunoglobulin superfamily.

[0075] Ligand-immunoglobulin chimeras are also known, and are disclosed, for example, in U.S. Patents Nos. 5,304,640 (for L-selectin ligands); 5,316,921 and 5,328,837 (for HGF variants). These chimeras can be made in a similar way to the construction of receptor-immunoglobulin chimeras.

[0076] Covalent modifications of the TIE ligand homologues of the present invention are included within the scope herein. Such modifications are traditionally introduced by reacting targeted amino acid residues of the TIE ligand with an organic derivatizing agent that is capable of reacting with selected sides or terminal residues, or by harnessing mechanisms of post-translational modifications that function in selected recombinant host cells. The resultant covalent derivatives are useful in programs directed at identifying residues important for biological activity, for immunoassays, or for the preparation of anti-TIE ligand antibodies for immunoaffinity purification of the recombinant. For example, complete inactivation of the biological activity of the protein after reaction with ninhydrin would suggest that at least one arginyl or lysyl residue is critical for its activity, whereafter the individual residues which were modified under the conditions selected are identified by isolation of a peptide fragment containing the modified amino acid residue. Such modifications are within the ordinary skill in the art and are performed without undue experimentation.

[0077] Cysteiny residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteiny residues also are derivatized by reaction with bromotrifluoroacetone, α -bromo- β -(5-imidazolyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

[0078] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0.

[0079] Lysiny and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysiny residues. Other suitable reagents for derivatizing α -amino-containing residues include imidoesters such as methyl picolinimate; pyridoxal phosphate; pyridoxal: chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0080] Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pK_a of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0081] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetyl-imidazole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay.

[0082] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides ($R'-N=C=N-R'$) such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginy and glutaminy residues by reaction with ammonium ions.

[0083] Glutaminy and asparaginy residues are frequently deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0084] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threony or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 [1983]), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group. The molecules may further be covalently linked to nonproteinaceous polymers, e.g. polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. patents 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

[0085] Derivatization with bifunctional agents is useful for preparing intramolecular aggregates of the TIE ligand with polypeptides as well as for cross-linking the TIE ligand polypeptide to a water insoluble support matrix or surface for use

in assays or affinity purification. In addition, a study of interchain cross-links will provide direct information on conformational structure. Commonly used cross-linking agents include 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, homobifunctional imidoesters, and bifunctional maleimides. Derivatizing agents such as methyl-3-1(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates which are capable of forming cross-

links in the presence of light. Alternatively, reactive water insoluble matrices such as cyanogen bromide activated carbohydrates and the systems reactive substrates described in U.S. Patent Nos. 3,959,642; 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; 4,055,635; and 4,330,440 are employed for protein immobilization and cross-linking.

[0086] Certain post-translational modifications are the result of the action of recombinant host cells on the expressed polypeptide. Glutaminyl and asparaginyl residues are frequently post-translationally deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[0087] Other post-translational modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)].

[0088] Other derivatives comprise the novel peptides of this invention covalently bonded to a nonproteinaceous polymer. The nonproteinaceous polymer ordinarily is a hydrophilic synthetic polymer, i.e. a polymer not otherwise found in nature. However, polymers which exist in nature and are produced by recombinant or *in vitro* methods are useful, as are polymers which are isolated from nature. Hydrophilic polyvinyl polymers fall within the scope of this invention, e.g. polyvinylalcohol and polyvinylpyrrolidone. Particularly useful are polyvinylalkylene ethers such as polyethylene glycol, polypropylene glycol.

[0089] The TIE ligand homologues may be linked to various nonproteinaceous polymers, such as polyethylene glycol (PEG), polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. These variants, just as the immunoadhesins of the present invention are expected to have longer half-lives than the corresponding native TIE ligand homologues.

[0090] The TIE ligand homologues may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, in colloidal drug delivery systems (e.g. liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th Edition, Osol, A., Ed. (1980).

[0091] The term "native TIE receptor" is used herein to refer to a TIE receptor of any animal species, including, but not limited to, humans, other higher primates, e.g. monkeys, and rodents, e.g. rats and mice, known or hereinafter discovered. The definition specifically includes the TIE-2 receptor, disclosed, for example, in PCT Application Serial No. WO 95/13387 (published 18 May 1995), and the endothelial cell receptor tyrosine kinase termed "TIE" in PCT Application Publication No. WO 93/14124 (published 22 July 1993), and preferably is TIE-2.

B. ANTI-TIE LIGAND HOMOLOGUE ANTIBODIES

[0092] The present invention covers antibodies specifically binding the TIE ligand homologues. The antibodies may be monoclonal or polyclonal, and include, without limitation, mature antibodies, antibody fragments (e.g. Fab, F(ab')₂, F_v, etc.), single-chain antibodies and various chain combinations.

[0093] The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies specifically binding a TIE ligand of the present invention and antibody compositions with polyeptopic specificity.

[0094] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen.

[0095] The monoclonal antibodies herein include hybrid and recombinant antibodies produced by splicing a variable (including hypervariable) domain of an anti-TIE ligand homologue antibody with a constant domain (e.g. "humanized" antibodies), or a light chain with a heavy chain, or a chain from one species with a chain from another species, or fusions with heterologous proteins, regardless of species of origin or immunoglobulin class or subclass designation, as well as antibody fragments (e.g. Fab, F(ab')₂, and F_v), so long as they exhibit the desired biological activity. See, e.g. U.S. Pat. No. 4,816,567 and Mage et al., in Monoclonal Antibody Production Techniques and Applications, pp. 79-97 (Marcel Dekker, Inc.: New York, 1987).

[0096] Thus the modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by

the hybridoma method first described by Kohler and Milstein, Nature, 256:495 (1975), or may be made by recombinant DNA methods such as described in U.S. Pat. No. 4,816,567. The "monoclonal antibodies" may also be isolated from phage libraries generated using the techniques described in McCafferty et al., Nature, 348:552-554 (1990), for example.

[0097] "Humanized" forms of non-human (e.g. murine) antibodies are specific chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, the humanized antibody may comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and optimize antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region or domain (Fc), typically that of a human immunoglobulin.

[0098] Polyclonal antibodies to a TIE ligand homologue of the present invention generally are raised in animals by multiple subcutaneous (sc) or intraperitoneal (ip) injections of the TIE ligand and an adjuvant. It may be useful to conjugate the TIE ligand or a fragment containing the target amino acid sequence to a protein that is immunogenic in the species to be immunized, e.g. keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, or soybean trypsin inhibitor using a bifunctional or derivatizing agent, for example maleimidobenzoyl sulfosuccinimide ester (conjugation through cysteine residues), N-hydroxysuccinimide (through lysine residues), glytaraldehyde, succinic anhydride, SOCl₂, or R¹N=C=NR, where R and R¹ are different alkyl groups.

[0099] Animals are immunized against the immunogenic conjugates or derivatives by combining 1 mg or 1 µg of conjugate (for rabbits or mice, respectively) with 3 volumes of Freud's complete adjuvant and injecting the solution intradermally at multiple sites. One month later the animals are boosted with 1/5 to 1/10 the original amount of conjugate in Freud's complete adjuvant by subcutaneous injection at multiple sites. 7 to 14 days later the animals are bled and the serum is assayed for anti-TIE ligand antibody titer. Animals are boosted until the titer plateaus. Preferably, the animal boosted with the conjugate of the same TIE ligand, but conjugated to a different protein and/or through a different cross-linking reagent. Conjugates also can be made in recombinant cell culture as protein fusions. Also, aggregating agents such as alum are used to enhance the immune response.

[0100] Monoclonal antibodies are obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies.

[0101] For example, the anti-TIE ligand homologue monoclonal antibodies of the invention may be made using the hybridoma method first described by Kohler & Milstein, Nature 256:495 (1975), or may be made by recombinant DNA methods [Cabilly, *et al.*, U.S. Pat. No. 4,816,567].

[0102] In the hybridoma method, a mouse or other appropriate host animal, such as hamster is immunized as hereinabove described to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)).

[0103] The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which substances prevent the growth of HGPRT-deficient cells.

[0104] Preferred myeloma cells are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Among these, preferred myeloma cell lines are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, California USA, and SP-2 cells available from the American Type Culture Collection, Rockville, Maryland USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol. 133:3001 (1984); Brodeur, *et al.*, Monoclonal Antibody Production Techniques and Applications, pp.51-63 (Marcel Dekker, Inc., New York, 1987)].

[0105] Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the TIE ligand homologue. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA)

or enzyme-linked immunoabsorbent assay (ELISA).

[0106] The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson & Pollard, *Anal. Biochem.* 107:220 (1980).

[0107] After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods. Goding, *Monoclonal Antibodies: Principles and Practice*, pp.59-104 (Academic Press, 1986). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal.

[0108] The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0109] DNA encoding the monoclonal antibodies of the invention is readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences, Morrison, *et al.*, *Proc. Nat. Acad. Sci.* 81, 6851 (1984), or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. In that manner, "chimeric" or "hybrid" antibodies are prepared that have the binding specificity of an anti-TIE ligand monoclonal antibody herein.

[0110] Typically such non-immunoglobulin polypeptides are substituted for the constant domains of an antibody of the invention, or they are substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for a TIE ligand of the present invention and another antigen-combining site having specificity for a different antigen.

[0111] Chimeric or hybrid antibodies also may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate.

[0112] For diagnostic applications, the antibodies of the invention typically will be labeled with a detectable moiety. The detectable moiety can be any one which is capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin; biotin; radioactive isotopic labels, such as, e.g., ^{125}I , ^{32}P , ^{14}C , or ^3H , or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase.

[0113] Any method known in the art for separately conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter, *et al.*, *Nature* 144:945 (1962); David, *et al.*, *Biochemistry* 13:1014 (1974); Pain, *et al.*, *J. Immunol. Meth.* 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.* 30:407 (1982).

[0114] The antibodies of the present invention may be employed in any known assay method, such as competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays. Zola, *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158 (CRC Press, Inc., 1987).

[0115] Competitive binding assays rely on the ability of a labeled standard (which may be a TIE ligand homologue or an immunologically reactive portion thereof) to compete with the test sample analyte (TIE ligand) for binding with a limited amount of antibody. The amount of TIE ligand homologue in the test sample is inversely proportional to the amount of standard that becomes bound to the antibodies. To facilitate determining the amount of standard that becomes bound, the antibodies generally are insolubilized before or after the competition, so that the standard and analyte that are bound to the antibodies may conveniently be separated from the standard and analyte which remain unbound.

[0116] Sandwich assays involve the use of two antibodies, each capable of binding to a different immunogenic portion, or epitope, of the protein to be detected. In a sandwich assay, the test sample analyte is bound by a first antibody which is immobilized on a solid support, and thereafter a second antibody binds to the analyte, thus forming an insoluble three part complex. David & Greene, U.S. Pat No. 4,376,110. The second antibody may itself be labeled with a detectable moiety (direct sandwich assays) or may be measured using an anti-immunoglobulin antibody that is labeled with a detectable moiety (indirect sandwich assay). For example, one type of sandwich assay is an ELISA assay, in which case the detectable moiety is an enzyme.

[0117] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain.

Humanization can be essentially performed following the method of Winter and co-workers Jones *et al.*, Nature **321**, 522-525 (1986); Riechmann *et al.*, Nature **332**, 323-327 (1988); Verhoeven *et al.*, Science **239**, 1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (Cabilly, *supra*), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0118] It is important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three dimensional models of the parental and humanized sequences. Three dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e. the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the consensus and import sequence so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

[0119] Alternatively, it is now possible to produce transgenic animals (e.g mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, e.g. Jakobovits *et al.*, Proc. Natl. Acad. Sci. USA **90**, 2551-2555 (1993); Jakobovits *et al.*, Nature **362**, 255-258 (1993).

[0120] Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for a particular TIE ligand, the other one is for any other antigen, and preferably for another ligand. For example, bispecific antibodies specifically binding two different TIE ligand homologues are within the scope of the present invention.

[0121] Methods for making bispecific antibodies are known in the art.

[0122] Traditionally, the recombinant production of bispecific antibodies is based on the coexpression of two immunoglobulin heavy chain-light chain pairs, where the two heavy chains have different specificities (Millstein and Cuello, Nature **305**, 537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in PCT application publication No. WO 93/08829 (published 13 May 1993), and in Traunecker *et al.*, EMBO **10**, 3655-3659 (1991).

[0123] According to a different and more preferred approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy chain constant domain, comprising at least part of the hinge, and second and third constant regions of an immunoglobulin heavy chain (CH2 and CH3). It is preferred to have the first heavy chain constant region (CH1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are cotransfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance. In preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecule provides for a facile way of separation.

[0124] For further details of generating bispecific antibodies see, for example, Suresh *et al.*, Methods in Enzymology **121**, 210 (1986),

[0125] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain ($V_H - V_L$). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains

are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404.097; WO 93/11161; and Hollinger *et al.*, Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

[0126] An "isolated" antibody is defined similarly to the definition provided hereinabove for isolated polypeptides. Specifically, an "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0127] The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

[0128] By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., control led pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate: in others it is a purification-column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

[0129] A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as the anti-ErbB2 antibodies disclosed herein and, optionally, a chemotherapeutic agent) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

[0130] Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (PCT application publication Nos. WO 91/00360 and WO 92/200373; EP 03089) Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Patent No. 4,676,980, along with a number of cross-linking techniques.

[0131] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

C. CLONING AND EXPRESSION OF THE TIE LIGAND HOMOLOGUES

[0132] In the context of the present invention the expressions "cell", "cell line", and "cell culture" are used interchangeably, and all such designations include progeny. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same function or biological property, as screened for in the originally transformed cell, are included.

[0133] The terms "replicable expression vector" and "expression vector" refer to a piece of DNA, usually double-stranded, which may have inserted into it a piece of foreign DNA. Foreign DNA is defined as heterologous DNA, which is DNA not naturally found in the host cell. The vector is used to transport the foreign or heterologous DNA into a suitable host cell. Once in the host cell, the vector can replicate independently of the host chromosomal DNA, and several copies of the vector and its inserted (foreign) DNA may be generated. In addition, the vector contains the necessary elements that permit translating the foreign DNA into a polypeptide. Many molecules of the polypeptide encoded by the foreign DNA can thus be rapidly synthesized.

[0134] Expression and cloning vectors are well known in the art and contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. The selection of the appropriate vector will depend on 1) whether it is to be used for DNA amplification or for DNA expression, 2) the size of the DNA to be inserted into the vector, and 3) the host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and the host cell for which it is compatible. The vector components generally

include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence.

(i) Signal Sequence Component

[0135] In general, the signal sequence may be a component of the vector, or it may be a part of the TIE ligand molecule that is inserted into the vector. If the signal sequence is heterologous, it should be selected such that it is recognized and processed (i.e. cleaved by a signal peptidase) by the host cell.

[0136] Heterologous signal sequences suitable for prokaryotic host cells are preferably prokaryotic signal sequences, such as the α -amylase, ompA, ompC, ompE, ompF, alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the yeast invertase, amylase, alpha factor, or acid phosphatase leaders may, for example, be used. In mammalian cell expression mammalian signal sequences are most suitable. The listed signal sequences are for illustration only, and do not limit the scope of the present invention in any way.

(ii) Origin of Replication Component

[0137] Both expression and cloning vectors contain a nucleic acid sequence that enabled the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomes, and includes origins of replication or autonomously replicating sequences. Such sequence are well known for a variety of bacteria, yeast and viruses. The origin of replication from the well-known plasmid pBR322 is suitable for most gram negative bacteria, the μ plasmid origin for yeast and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. Origins of replication are not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter). Most expression vectors are "shuttle" vectors, i.e. they are capable of replication in at least one class of organisms but can be transfected into another organism for expression. For example, a vector is cloned in *E. coli* and then the same vector is transfected into yeast or mammalian cells for expression even though it is not capable of replicating independently of the host cell chromosome.

[0138] DNA is also cloned by insertion into the host genome. This is readily accomplished using *Bacillus* species as hosts, for example, by including in the vector a DNA sequence that is complementary to a sequence found in *Bacillus* genomic DNA. Transfection of *Bacillus* with this vector results in homologous recombination with the genome and insertion of the DNA encoding the desired heterologous polypeptide. However, the recovery of genomic DNA is more complex than that of an exogenously replicated vector because restriction enzyme digestion is required to excise the encoded polypeptide molecule.

(iii) Selection Gene Component

[0139] Expression and cloning vectors should contain a selection gene, also termed a selectable marker. This is a gene that encodes a protein necessary for the survival or growth of a host cell transformed with the vector. The presence of this gene ensures that any host cell which deletes the vector will not obtain an advantage in growth or reproduction over transformed hosts. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g. ampicillin, neomycin, methotrexate or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g. the gene encoding D-alanine racemase for bacilli.

[0140] One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene express a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin [Southern *et al.*, *J. Molec. Appl. Genet.* **1**, 327 (1982)], mycophenolic acid [Mulligan *et al.*, *Science* **209**, 1422 (1980)], or hygromycin [Sudgen *et al.*, *Mol. Cell. Biol.* **5**, 410-413 (1985)]. The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug G418 or neomycin (geneticin), xgpt (mycophenolic acid), or hygromycin, respectively.

[0141] Other examples of suitable selectable markers for mammalian cells are dihydrofolate reductase (DHFR) or thymidine kinase. Such markers enable the identification of cells which were competent to take up the desired nucleic acid. The mammalian cell transformants are placed under selection pressure which only the transformants are uniquely adapted to survive by virtue of having taken up the marker. Selection pressure is imposed by culturing the transformants under conditions in which the concentration of selection agent in the medium is successively changed, thereby leading to amplification of both the selection gene and the DNA that encodes the desired polypeptide. Amplification is the process by which genes in greater demand for the production of a protein critical for growth are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Increased quantities of the desired polypeptide are synthesized from the amplified DNA.

[0142] For example, cells transformed with the DHFR selection gene are first identified by culturing all of the trans-

formants in a culture medium which lacks hypoxanthine, glycine, and thymidine. An appropriate host cell in this case is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity, prepared and propagated as described by Urlaub and Chasin, *Proc. Nat'l. Acad. Sci. USA* 77, 4216 (1980). A particularly useful DHFR is a mutant DHFR that is highly resistant to MTX (EP 117,060). This selection agent can be used with any otherwise suitable host. e.g. ATCC No. CCL61 CHO-K1, notwithstanding the presence of endogenous DHFR. The DNA encoding DHFR and the desired polypeptide, respectively, then is amplified by exposure to an agent (methotrexate, or MTX) that inactivates the DHFR. One ensures that the cell requires more DHFR (and consequently amplifies all exogenous DNA) by selecting only for cells that can grow in successive rounds of ever-greater MTX concentration. Alternatively, hosts co-transformed with genes encoding the desired polypeptide, wild-type DHFR, and another selectable marker such as the neo gene can be identified using a selection agent for the selectable marker such as G4 18 and then selected and amplified using methotrexate in a wild-type host that contains endogenous DHFR. (See also U.S. Patent No. 4,965,199).

[0143] A suitable selection gene for use in yeast is the trp1 gene present in the yeast plasmid YRp7 (Stinchcomb *et al.*, 1979, *Nature* 282:39; Kingsman *et al.*, 1979, *Gene* 7:14 1; or Tschemper *et al.*, 1980, *Gene* 10: 157). The trp1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 (Jones, 1977, *Genetics* 85: 12). The presence of the trp1 lesion in the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan. Similarly, Leu2 deficient yeast strains (ATCC 20,622 or 38,626) are complemented by known plasmids bearing the Leu2 gene.

(iv) Promoter Component

[0144] Expression vectors, unlike cloning vectors, should contain a promoter which is recognized by the host organism and is operably linked to the nucleic acid encoding the desired polypeptide. Promoters are untranslated sequences located upstream from the start codon of a structural gene (generally within about 100 to 1000 bp) that control the transcription and translation of nucleic acid under their control. They typically fall into two classes, inducible and constitutive. Inducible promoters are promoters that initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, e.g. the presence or absence of a nutrient or a change in temperature. At this time a large number of promoters recognized by a variety of potential host cells are well known. These promoters are operably linked to DNA encoding the desired polypeptide by removing them from their gene of origin by restriction enzyme digestion, followed by insertion 5' to the start codon for the polypeptide to be expressed. This is not to say that the genomic promoter for a TIE ligand is not usable. However, heterologous promoters generally will result in greater transcription and higher yields of expressed TIE ligand homologues as compared to the native TIE ligand promoters.

[0145] Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems (Chang *et al.*, *Nature* 275:615 (1978); and Goeddel *et al.*, *Nature* 281:544 (1979)), alkaline phosphatase, a tryptophan (trp) promoter system (Goeddel, *Nucleic Acids Res.* 8:4057 (1980) and EPO Appln. Publ. No. 36,776) and hybrid promoters such as the tac promoter (H. de Boer *et al.*, *Proc. Nat'l. Acad. Sci. USA* 80:21-25 (1983)). However, other known bacterial promoters are suitable. Their nucleotide sequences have been published, thereby enabling a skilled worker operably to ligate them to DNA encoding a TIE ligand (Siebenlist *et al.*, *Cell* 20:269 (1980)) using linkers or adaptors to supply any required restriction sites. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding a TIE ligand.

[0146] Suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman *et al.* *J. Biol. Chem.* 255:2073 (1980)) or other glycolytic enzymes (Hess *et al.*, *J. Adv. Enzyme Reg.* 7:149 (1978); and Holland, *Biochemistry* 17:4900 (1978)). such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate-isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

[0147] Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman *et al.*, EP 73,657A. Yeast enhancers also are advantageously used with yeast promoters.

[0148] Promoter sequences are known for eukaryotes. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 bases upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of transcription of many genes is a CXCAAT region where X may be any nucleotide. At the 3' end of most eukaryotic genes is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3' end of the coding sequence. All of these sequences are suitably inserted into mammalian expression vectors.

[0149] TIE ligand transcription from vectors in mammalian host cells may be controlled by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most

preferably Simian Virus 40 (SV40) from heterologous mammalian promoters, e.g. the actin promoter or an immunoglobulin promoter, from heat shock promoters, and from the promoter normally associated with the TIE ligand sequence, provided such promoters are compatible with the host cell systems.

[0150] The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment which also contains the SV40 viral origin of replication [Fiers *et al.*, *Nature* 273:113 (1978), Mulligan and Berg, *Science* 209, 1422-1427 (1980); Pavlakis *et al.*, *Proc. Natl. Acad. Sci. USA* 78, 7398-7402 (1981)]. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment (Greenaway *et al.*, *Gene* 18, 355-360 (1982)]. A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in US 4,419,446. A modification of this system is described in US 4,601,978. See also, Gray *et al.*, *Nature* 295, 503-508 (1982) on expressing cDNA encoding human immune interferon in monkey cells; Reyes *et al.*, *Nature* 297, 598-601 (1982) on expressing human β -interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus; Canaani and Berg, *Proc. Natl. Acad. Sci. USA* 79, 5166-5170 (1982) on expression of the human interferon β 1 gene in cultured mouse and rabbit cells; and Gorman *et al.*, *Proc. Natl. Acad. Sci. USA* 79, 6777-6781 (1982) on expression of bacterial CAT sequences in CV-1 monkey kidney cells, chicken embryo fibroblasts, Chinese hamster ovary cells, HeLa cells, and mouse HIN-3T3 cells using the Rous sarcoma virus long terminal repeat as a promoter.

(v) Enhancer Element Component

[0151] Transcription of a DNA encoding the TIE ligand homologues of the present invention by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Enhancers are relatively orientation and position independent having been found 5' [Laimins *et al.*, *Proc. Natl. Acad. Sci. USA* 78, 993 (1981)] and 3' [Lasky *et al.*, *Mol. Cell., Biol.* 3, 1108 (1983)] to the transcription unit, within an intron [Banerji *et al.*, *Cell* 33, 729 (1983)] as well as within the coding sequence itself [Osborne *et al.*, *Mol. Cell., Biol.* 4, 1293 (1984)]. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter/enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, *Nature* 297, 17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5' or 3' to the TIE ligand DNA, but is preferably located at a site 5' from the promoter.

(vi) Transcription Termination Component

[0152] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3' untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding the TIE ligand. The 3' untranslated regions also include transcription termination sites.

[0153] Construction of suitable vectors containing one or more of the above listed components, the desired coding and control sequences, employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to generate the plasmids required.

[0154] For analysis to confirm correct sequences in plasmids constructed, the ligation mixtures are used to transform *E. coli* K 12 strain 294 (ATCC 31,446) and successful transformants selected by ampicillin or tetracycline resistance where appropriate. Plasmids from the transformants are prepared, analyzed by restriction endonuclease digestion, and/or sequenced by the method of Messing *et al.*, *Nucleic Acids Res.* 9, 309 (1981) or by the method of Maxam *et al.*, *Methods in Enzymology* 65, 499 (1980).

[0155] Particularly useful in the practice of this invention are expression vectors that provide for the transient expression in mammalian cells of DNA encoding a TIE ligand. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high levels of a desired polypeptide encoded by the expression vector. Transient systems, comprising a suitable expression vector and a host cell, allow for the convenient positive identification of polypeptides encoded by clones DNAs, as well as for the rapid screening of such polypeptides for desired biological or physiological properties. Thus, transient expression systems are particularly useful in the invention for purposes of identifying analogs and variants of a TIE ligand.

[0156] Other methods, vectors, and host cells suitable for adaptation to the synthesis of the TIE polypeptides in recombinant vertebrate cell culture are described in Gening *et al.*, *Nature* 293, 620-625 (1981); Mantel *et al.*, *Nature*

281, 40-46 (1979); Levinson *et al.*; EP 117,060 and EP 117,058. A particularly useful plasmid for mammalian cell culture expression of the TIE ligand polypeptides is pRK5 (EP 307,247). along with its derivatives, such as, pRK5D that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the Xho/NotII cDNA cloning sites, and pRK5B, a precursor of pRK5D that does not contain the SfiI site; see, Holmes *et al.*, Science 253, 1278-1280 (1991).

(vii) Construction and analysis of vectors

[0157] Construction of suitable vectors containing one or more of the above listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and religated in the form desired to generate the plasmids required.

[0158] For analysis to confirm correct sequences in plasmids constructed, the ligation mixtures are used to transform *E. coli* K 12 strain 294 (ATCC 31,446) and successful transformants selected by ampicillin or tetracycline resistance where appropriate. Plasmids from the transformants are prepared, analyzed by restriction endonuclease digestion, and/or sequences by the methods of Messing *et al.*, Nucleic Acids Res. 9,309 (1981) or by the method of Maxam *et al.*, Methods in Enzymology 65, 499 (1980).

(viii) Transient expression vectors

[0159] Particularly useful in the practice of this invention are expression vectors that provide for the transient expression in mammalian cells of DNA encoding a TIE ligand. In general, transient expression involves the use of an expression vector that is able to replicate efficiently in a host cell, such that the host cell accumulates many copies of the expression vector and, in turn, synthesizes high level of a desired polypeptide encoded by the expression vector. Sambrook *et al.*, supra, pp. 16.17-16.22. Transient expression systems, comprising a suitable expression vector and a host cell, allow for the convenient positive screening of such polypeptides for desired biological or physiological properties. Thus transient expression systems are particularly useful in the invention for purposes of identifying analogs and variants of native TIE ligand homologues with the requisite biological activity.

(ix) Suitable exemplary vertebrate cell vectors

[0160] Other methods, vectors, and host cells suitable for adaptation to the synthesis of a TIE ligand (including functional derivatives of native proteins) in recombinant vertebrate cell culture are described in Gething *et al.*, Nature 293, 620-625 (1981); Mantei *et al.*, Nature 281, 40-46 (1979); Levinson *et al.*, EP 117,060; and EP 117,058. A particularly useful plasmid for mammalian cell culture expression of a TIE ligand is pRK5 (EP 307,247) or pSV16B (PCT Publication No. WO 91/08291).

[0161] Suitable host cells for cloning or expressing the vectors herein are the prokaryote, yeast or higher eukaryote cells described above. Suitable prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. A preferred cloning host is *E. coli* 294 (ATCC 31,446) although other gram negative or gram positive prokaryotes such as *E. coli* B, *E. coli* X1776 (ATCC 31,537), *E. coli* W3110 (ATCC 27,325), *Pseudomonas* species, or *Serratia Marcesans* are suitable.

[0162] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable hosts for vectors herein. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species and strains are commonly available and useful herein, such as *S. pombe* [Beach and Nurse, Nature 290, 140 (1981)], *Kluyveromyces fragilis* [Louvencourt *et al.*, J. Bacteriol. 737(1983)]; *varrowia* (EP402,226); *Pichia pastoris* (EP 183.070), *Trichoderma reesei* (EP244,234), *Neurospora crassa* [Case *et al.*, Proc.Natl. Acad. Sci. USA 76, 5259-5263(1979)]; and *Aspergillus* hosts such as *A. nidulans* [Ballance *et al.*, Biochem. Biophys. Res. Commun. 112, 284-289(1983); Tilburn *et al.*, Gene 26, 205-221 (1983); Yelton *et al.*, Proc. Natl. Acad. Sci. USA 81, 1470-1474 (1984)] and *A. niger* [Kelly and Hynes, EMBO J. 4,475-479 (1985)].

[0163] Suitable host cells may also derive from multicellular organisms. Such host cells are capable of complex processing and glycosylation activities. In principle, any higher eukaryotic cell culture is workable, whether from vertebrate or invertebrate culture, although cells from mammals such as humans are preferred. Examples of invertebrate cells include plants and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *O Bombyx mori* host cells have been identified. See, e.g. Luckow *et al.*, Bio/Technology 6, 47-55 (1988); Miller *et al.*, in Genetic Engineering, Setlow, J.K. *et al.*, eds., Vol. 8 (Plenum Publishing, 1986), pp. 277-279; and Maeda *et al.*, Nature 315, 592-594 (1985). A variety of such viral strains are publicly available, e.g. the L-1 variant of *Autographa californica* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

[0164] Generally, plant cells are transfected by incubation with certain strains of the bacterium *Agrobacterium tumefaciens*.

faciens, which has been previously manipulated to contain the TIE ligand DNA. During incubation of the plant cell culture with A. tumefaciens, the DNA encoding a TIE ligand is transferred to the plant cell host such that it is transfected, and will, under appropriate conditions, express the TIE ligand DNA. In addition, regulatory and signal sequences compatible with plant cells are available, such as the nopaline synthase promoter and polyadenylation signal sequences. Depicker *et al.*, J. Mol. Appl. Gen **1**, 561 (1982). In addition, DNA segments isolated from the upstream region of the T-DNA 780 gene are capable of activating or increasing transcription levels of plant-expressible genes in recombinant DNA-containing plant tissue. See EP 321,196 published 21 June 1989.

[0165] However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) is per se well known. See Tissue Culture, Academic Press, Kruse and Panerson, editors (1973). Examples of useful mammalian host cell lines are monkey kidney CV 1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney cell line [293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, J. Gen. Virol. **36**, 59 (1977)]; baby hamster kidney cells 9BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR [CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA **77**, 4216 (1980)]; mouse sertoli cells [TM4, Mather, Biol. Reprod. **23**, 243-251 (1980)]; monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W 138, ATCC CCL75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562 ATCC CCL51)-, TRI cells [Mather *et al.*, Annals N.Y. Acad. Sci. **383**, 44068 (1982)]; MRC 5 cells; FS4 cells; and a human hepatoma cell line (Hep G2). Preferred host cells are human embryonic kidney 293 and Chinese hamster ovary cells.

[0166] Particularly preferred host cells for the purpose of the present invention are vertebrate cells producing the TIE ligand homologues of the present invention.

[0167] Host cells are transfected and preferably transformed with the above-described expression or cloning vectors and cultured in conventional nutrient media modified as is appropriate for inducing promoters or selecting transformants containing amplified genes.

[0168] Prokaryotes cells used to produce the TIE ligand homologues of this invention are cultured in suitable media as describe generally in Sambrook *et al.*, supra.

[0169] Mammalian cells can be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium (MEM, Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium (DMEM, Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham and Wallace, Meth. Enzymol. **58**, 44 (1979); Barnes and Sato, Anal. Biochem. **102**, 255 (1980), US 4,767,704; 4,657,866; 4,927,762; or 4,560,655; WO 90/03430; WO 87/00195 or US Pat. Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleosides (such as adenosine and thymidine), antibiotics (such as Gentamycin™ drug) trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH and the like, suitably are those previously used with the host cell selected for cloning or expression, as the case may be, and will be apparent to the ordinary artisan.

[0170] The host cells referred to in this disclosure encompass cells in *in vitro* cell culture as well as cells that are within a host animal or plant.

[0171] It is further envisioned that the TIE ligand homologues of this invention may be produced by homologous recombination, or with recombinant production methods utilizing control elements introduced into cells already containing DNA encoding the particular TIE ligand.

[0172] Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA **77**, 5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Various labels may be employed, most commonly radioisotopes, particularly ³²P. However, other techniques may also be employed, such as using biotin-modified nucleotides for introduction into a polynucleotide. The biotin then serves as a site for binding to avidin or antibodies, which may be labeled with a wide variety of labels, such as radionuclides, fluorescers, enzymes, or the like. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to the surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

[0173] Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. With immunohistochemical staining techniques, a cell sample is prepared, typically by dehydration and fixation, followed by reaction with labeled antibodies specific for the gene product coupled, where the labels are usually visually detectable,

such as enzymatic labels, fluorescent labels, luminescent labels, and the like. A particularly sensitive staining technique suitable for use in the present invention is described by Hse *et al.*, *Am. J. Clin. Pharm.* 75, 734-738 (1980).

[0174] Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any animal. Conveniently, the antibodies may be prepared against a native TIE ligand polypeptide of the present invention, or against a synthetic peptide based on the DNA sequence provided herein as described further hereinbelow.

[0175] The TIE ligand homologue may be produced in host cells in the form of inclusion bodies or secreted into the periplasmic space or the culture medium, and is typically recovered from host cell lysates. The recombinant ligand homologues may be purified by any technique allowing for the subsequent formation of a stable protein.

[0176] When the TIE ligand homologue is expressed in a recombinant cell other than one of human origin, it is completely free of proteins or polypeptides of human origin. However, it is necessary to purify the TIE ligand homologue from recombinant cell proteins or polypeptides to obtain preparations that are substantially homogenous as to the ligand. As a first step, the culture medium or lysate is centrifuged to remove particulate cell debris. The membrane and soluble protein fractions are then separated. The TIE ligand homologue may then be purified from the soluble protein fraction. The following procedures are exemplary of suitable purification procedures: fractionation on immunoaffinity or ion-exchange columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; and protein A Sepharose columns to remove contaminants such as IgG.

[0177] Functional derivatives of the TIE ligand homologues in which residues have been deleted, inserted and/or substituted are recovered in the same fashion as the native ligands, taking into account of any substantial changes in properties occasioned by the alteration. For example, fusion of the TIE ligand homologue with another protein or polypeptide, e.g. a bacterial or viral antigen, facilitates purification; an immunoaffinity column containing antibody to the antigen can be used to absorb the fusion. Immunoaffinity columns such as a rabbit polyclonal anti-TIE ligand homologue column can be employed to absorb TIE ligand homologue variants by binding to at least one remaining immune epitope. A protease inhibitor, such as phenyl methyl sulfonyl fluoride (PMSF) also may be useful to inhibit proteolytic degradation during purification, and antibiotics may be included to prevent the growth of adventitious contaminants. The TIE ligand homologues of the present invention are conveniently purified by affinity chromatography, based upon their ability to bind to a TIE receptor, e.g. TIE-2.

[0178] One skilled in the art will appreciate that purification methods suitable for native TIE ligand homologues may require modification to account for changes in the character of a native TIE ligand homologue or its variants upon expression in recombinant cell culture

D. USE OF THE TIE LIGAND HOMOLOGUES, NUCLEIC ACID MOLECULES AND ANTIBODIES

[0179] The TIE ligand homologues of the present invention are expected to be useful in promoting the survival and/or growth and/or differentiation of TIE receptor expressing cells in cell culture.

[0180] The TIE ligand homologues may be additionally used to identify cells which express native TIE receptors. To this end, a detectably labeled ligand is contacted with a target cell under condition permitting its binding to its receptors (TIE receptor), and the binding is monitored.

[0181] The TIE ligand homologues herein may also be used to identify molecules exhibiting a biological activity of a TIE ligand homologue, for example, by exposing a cell expressing a TIE ligand homologue herein to a test molecule, and detecting the specific binding of the test molecule to a TIE receptor, either by direct detection, or based upon secondary biological effects. This approach is particularly suitable for identifying new members of the TIE ligand family, or for screening peptide or non-peptide small molecule libraries.

[0182] The TIE ligand homologues disclosed herein are also useful in screening assays designed to identify agonists or antagonists of a native TIE receptor that play an important role in bone development, maturation or growth, or in muscle growth or development and/or promote or inhibit angiogenesis. For example, antagonists of a TIE receptor may be identified based upon their ability to block the binding of a TIE ligand homologue of the present invention to a native TIE receptor, as measured, for example, by using BiAcCore biosensor technology (BiAcCore; Pharmacia Biosensor, Midscataway, N.J.); or by monitoring their ability to block the biological response caused by a biologically active TIE ligand homologue herein. Biological responses that may be monitored include, for example, the phosphorylation of the TIE receptor or downstream components of the TIE signal transduction pathway, or survival, growth or differentiation of cells expressing the TIE receptor. Cell-based assays, utilizing cells that do not normally the TIE receptor, engineered to express this receptor, or to coexpress the TIE receptor and a TIE ligand homologue of the present invention, are particularly convenient to use.

[0183] In a particular embodiment, small molecule agonists and antagonists of a native TIE receptor can be identified, based upon their ability to interfere with the TIE ligand/TIE receptor interaction. There are numerous ways for measuring the specific binding of a test molecule to a TIE receptor, including, but not limited to detecting or measuring the amount

of a test molecule bound to the surface of intact cells expressing the TIE receptor, cross-linked to the TIE receptor in cell lysates, or bound to the TIE receptor *in vitro*.

[0184] Detectably labeled TIE ligand homologues include, for example, TIE ligand homologues covalently or non-covalently linked to a radioactive substance, e.g. ^{125}I , a fluorescent substance, a substance having enzymatic activity (preferably suitable for colorimetric detection), a substrate for an enzyme (preferably suitable for colorimetric detection), or a substance that can be recognized by a(n) (detectably labeled) antibody molecule.

[0185] The assays may be performed in a manner similar to that described in PCT Publication WO 96/11269, published 18 April 1996.

[0186] The TIE ligand homologues of the present invention are also useful for purifying TIE receptors, optionally used in the form of immunoadhesins, in which the TIE ligand or the TIE receptor binding portion thereof is fused to an immunoglobulin heavy or light chain constant region.

[0187] In addition, the new TIE ligand homologues herein may be useful for inhibiting tumor growth.

[0188] The nucleic acid molecules of the present invention are useful for detecting the expression of TIE ligand homologues in cells or tissue sections. Cells or tissue sections may be contacted with a detectably labeled nucleic acid molecule encoding a TIE ligand of the present invention under hybridizing conditions, and the presence of mRNA hybridized to the nucleic acid molecule determined, thereby detecting the expression of the TIE ligand.

[0189] Antibodies of the present invention may, for example, be used in immunoassays to measure the amount of a TIE ligand in a biological sample. The biological sample is contacted with an antibody or antibody mixture specifically binding the a TIE ligand of the present invention, and the amount of the complex formed with a ligand present in the test sample is measured.

[0190] Antibodies to the TIE ligand homologues herein may additionally be used for the delivery of cytotoxic molecules, e.g. radioisotopes or toxins, or therapeutic agents to cells expressing a corresponding TIE receptor. The therapeutic agents may, for example, be other TIE ligand homologues, including the TIE-2 ligand, members of the vascular endothelial growth factor (VEGF) family, or known anti-tumor agents, and agents known to be associated with muscle growth or development, or bone development, maturation, or growth.

[0191] For therapeutic use, the TIE ligand homologues or anti-TIE ligand antibodies of the present invention are formulated as therapeutic composition comprising the active ingredient(s) in admixture with a pharmacologically acceptable vehicle, suitable for systemic or topical application. The pharmaceutical compositions of the present invention are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's *Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecularweight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forminecounterionssuch as sodium; and/or nonionic surfactants such as Tween, Pluronic or PEG.

[0192] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(meth-ylmelhacyle)microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences*, *supra*.

[0193] The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

[0194] Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0195] The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intra-peritoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

[0196] Suitable examples of sustained release preparations include semipermeable polymer matrices in the form of shaped articles, e.g. films, or microcapsules. Sustained release matrices include polyesters, hydrogels, polylactides (U.S. Patent 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (U. Sidman *et al.*, 1983, "Biopolymers" 22 (1): 547-556), poly (2-hydroxyethylmethacrylate) (R. Langer, *et al.*, 1981, "J. Biomed. Mater. Res." 15: 167-277 and R. Langer, 1982, Chem. Tech." 12: 98-105), ethylene vinyl acetate (R. Langer *et al.*, *Id.*) or poly D-(-)-3-hydroxybutyric acid (EP 133,988A). Sustained release compositions also include liposomes. Liposomes containing a molecule within the scope of the present invention are prepared by methods known *per se*: DE 3,218,121 A; Epstein *et al.*, 1985, "Proc. Natl. Acad. Sci. USA" 82: 3688-3692; Hwang *et al.*, 1980, "Proc. Natl. Acad. Sci. USA" 77: 4030-4034; EP 52322A; EP 36676A; EP 88046A; EP 143949A; EP 142641A; Japanese patent application 83-118008;

U.S. patents 4,485,045 and 4,544,545; and EP 102.324A Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. % cholesterol, the selected proportion being adjusted for the optimal NT-4 therapy.

[0197] An effective amount of a molecule of the present invention to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage might range from about 1 µg/kg to up to 100 mg/kg or more, depending on the factors mentioned above. Typically, the clinician will administer a molecule of the present invention until a dosage is reached that provides the required biological effect. The progress of this therapy is easily monitored by conventional assays.

[0198] If the therapeutic goal is to prevent or treat tumors, the compounds herein may be combined with other therapies. For example, the patient to be treated with such anti-cancer agents may also receive radiation therapy. Alternatively, or in addition, a chemotherapeutic agent may be administered to the patient. Preparation and dosing schedules for such chemotherapeutic agents may be used according to manufacturers instructions or as determined empirically by the skilled practitioner. Preparation and dosing schedules for such chemotherapy are also described in *Chemotherapy Service* Ed., M.C. Perry, Williams & Wilkins, Baltimore, MD (1992). The chemotherapeutic agent may precede, or follow administration of the anti-tumor agent, or may be given simultaneously therewith.

[0199] It may be desirable to also administer antibodies against other tumor associated antigens, such as antibodies which bind to the ErbB2, EGFR, ErbB3, ErbB4, or vascular endothelial factor (VEGF). Alternatively, or in addition, two or more antibodies binding the same or two or more different antigens disclosed herein may be co-administered to the patient. Sometimes, it may be beneficial to also administer one or more cytokines to the patient. In a preferred embodiment, the anti-tumor compounds herein are co-administered with a further growth inhibitory agent.

[0200] For the prevention or treatment of disease, the appropriate dosage of an anti-tumor agent, e.g. an antibody herein will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the agent is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the agent, and the discretion of the attending physician. The agent is suitably administered to the patient at one time or over a series of treatments.

Example 1

Identification of NL3

[0201] NL3 was identified by screening the GenBank database using the computer program BLAST (Altshul et al., *Methods in Enzymology* 266:460-480 (1996).

[0202] NL3 shows homology with the known EST sequences T57280, and T50719. None of the known EST sequences have been identified as full length sequences, or described as ligands associated with the TIE receptors.

[0203] Following its identification NL3 was cloned from a human fetal lung library prepared from mRNA purchased from Clontech, Inc. (Palo Alto, CA. USA), catalog # 6528.1, following the manufacturer's instructions. The library was screened by hybridization with synthetic oligonucleotide probes:

[0204] For NL3:

NL3,5-1	TGGTTGGCAAAGGCAAGGTGGCTGACGATCCGG	SEQ. ID. NO: 10
NL3.3-1	GTGGCCCTTATCTCTCCTGTACAGCTTCCGGATCGTCAGCCAC	SEQ.ID.NO:11
NL3,3.2	TCCATTCCCACCTATGACGCTGACCCA	SEQ. ID. NO: 12

based on the ESTs found in the GenBank database. cDNA sequences were sequences in their entireties

[0205] The nucleotide and amino acid sequences of NL3 are shown in Figure 4 (SEQ. ID. NO: 3) and Figure 5 (SEQ. ID. NO: 4), respectively.

[0206] A clone of NL3 was deposited with the American Type Culture Collection (ATCC). 12301 Parklawn Drive, Rockville, Maryland 20852, on September 18, 1997 under the terms of the Budapest Treaty, and has been assigned the deposit number ATCC 209283.

Example 2

Northern Blot Analysis and *in situ* Hybridization Results

[0207] Expression of the NL3 mRNA in human tissues was examined by Northern blot analysis. Human mRNA blots were hybridized to a ³²P-labeled DNA probe based on the full length cDNAs; the probes were generated by digesting

and purifying the cDNA inserts. Human fetal RNA blot MTN - (Clontech) and human adult RNA blot MTN-II (Clontech) were incubated with the DNA probes. Blots were incubated with the probes in hybridization buffer (5x SSPE; 2Denhardt's solution; 100 mg/mL denatured sheared salmon sperm DNA; 50% formamide; 2% SDS) for 60 hours at 42°C. The blots were washed several times in 2x SSC; 0.05% SDS for 1 hour at room temperature, followed by a 30 minute wash in 0.1 x SSC; 0.1% SDS at 50°C. The blots were developed after overnight exposure by phosphorimager analysis (Fuji).

[0208] As shown in Figure 9, NL3 mRNA transcripts were detected.

[0209] The tissue expression pattern of NL3 was also determined by *in situ* hybridization (observing hybridization to cellular RNA), using an optimized protocol that employs PCR-generated ³³P-labeled riboprobes. (Lu and Gillett, *Cell Vision* 1: 169-176 (1994)). Formalin-fixed, paraffin-embedded human fetal and adult tissues were sectioned, deparaffinized, deproteinized in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett (1994). A [³³-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

³³P-Riboprobe synthesis

[0210] 6.0 µl (125 mCi) of ³³P-UTP (Amersham BF 1002, SA<2000 Ci/mmol) were speed vac dried. To each tube containing dried ³³P-UTP, the following ingredients were added:

- 2.0 µl 5x transcription buffer
- 1.0 µl DTT (100 mM)
- 2.0 µl NTP mix (2.5 mM : 10 µ; each of 10 mM GTP, CTP & ATP + 10 µl H₂O)
- 1.0 µl UTP (50 µM)
- 1.0 µl Rnasin
- 1.0 µl DNA template (1µg)
- 1.0 µl H₂O
- 1.0 µl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

[0211] The tubes were incubated at 37°C for one hour. 1.0 µl RQ1 DNase were added, followed by incubation at 37°C for 5 minutes. 90 µl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 µl TE were added. 1 µl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor 11.

[0212] The probe was run on a TBE/urea gel. 1-3 µl of the probe or 5 µl of RNA Mrk III were added to 3 µl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

³³P-Hybridization

[0213] *Pretreatment of frozen sections* The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde in ice in the fume hood, and washed in 0.5 x SSC for 5 minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H₂O). After deproteinization in 0.5 µg/ml proteinase K for 10 minutes at 37°C (12.5 µl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNase buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70%, 95%, 100% ethanol, 2 minutes each.

[0214] *Pretreatment of paraffin-embedded sections* The slides were deparaffinized, placed in SQ H₂O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinized in 20 µg/ml proteinase K (500 µl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 µl in 250 ml RNase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

[0215] *Prehybridization* The slides were laid out in plastic box lined with Box buffer (4 x SSC, 50% formamide) saturated filter paper. The tissue was covered with 50 µl of hybridization buffer (3.75g Dextran Sulfate+ 6 ml SQ H₂O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H₂O were added, the tissue was vortexed well, and incubated at 42°C for 1-4 hours.

[0216] *Hybridization* 1.0 x 10⁶ cpm probe and 1.0 µl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 µl hybridization buffer were added per slide. After vortexing, 50 µl ³³P mix were added to 50 µl prehybridization on slide. The slides were incubated overnight at 55°C.

[0217] Washes Washing was done 2x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, $V_f=4L$), followed by RNaseA treatment at 37°C for 30 minutes (500 μ l of 10 mg/m) in 250 ml Rnase buffer = 20 μ g/ml), The slides were washed 2x10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, $V_f=4L$)

Oligos:

[0218]

C-141 F - NL3pl: 48mer GGA TTC TAA TAC GAC TCA CTA TAG GGC AAG TTG TCC TCC
(SEQ ID NO: 16)

CGT C-141G - NL3p2: 47mer CTA TGA AAT TAA CCC TCA CTA AAG GGA CGT GGT CAG
(SEQ ID NO: 17)

[0219] The adult tissues examined were: liver, kidney, adrenal, myocardium, aorta, spleen, lympho node, pancreas, lung, skin, cerebral cortex, hippocampus, cerebellum, penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinomsa and chondrosarcoma, acetaminophen induced liver injury and hepatic cirrhosis. Fetal tissues examined were: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, penis and lower limb. Expression was not observed in any of the normal or fetal tissues. Expression was detected in hepatic sinusoidal cells (probably endothelial) in both acute (acetaminophen induced) and chronic hepatic injury (cirrhosis and adjacent to colorectal carcinoma metastasis). These results indicate that NL3 may play a role in the regulation of hepatic regeneration.

[0220] The expression of NL1 was also examined in a similar array of adult and fetal tissues but no expressed was observed under the conditions indicated above.

Example 3

Expression of NL 3 in *E. coli*

[0221] This example illustrates the preparation of an unglycosylated form of the TIE ligand homologues of the present invention in *E. coli*. The DNA sequence encoding a NL-3 ligand (SEQ. ID. NOs: 3 is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. The vector will preferably encode an antibiotic resistance gene, an origin of replication, e promoter, and a ribozyme binding site. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector.

[0222] The ligation mixture is then used to transform a selected *E. coli* strain, using the methods described in Sainbrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis.

[0223] Selected clones can be grown overnight in liquid culture medium such as 1B broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a later scale culture. The cells are then grown to a desired optical density. An inducer, such as IPTG may be added.

[0224] After culturing the cells for several more hours. the cells can be harvested by centrifugation The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

Example 4

Expression NL3 in mammalian cells

[0225] This example illustrates preparation of a glycosylated form of the NL3 ligand homologues by recombinant expression in mammalian cells.

[0226] The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the NL3 DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the NL3 DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-NL3.

[0227] In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown

to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-NL3 DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982) and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂). To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

[0228] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of NL3 polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

[0229] In an alternative technique, NL3 may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 µg pRK5-FLS139, -NL2 and -NL3 DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextranprecipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 µg/ml bovine insulin and 0.1 µg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed NL3 can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

[0230] In another embodiment, NL3 can be expressed in CHO cells. pRK5-NL3 can be transfected into CHO cells using known reagents such as CaPO₄ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ³⁵S-methionine. After determining the presence of NL3 polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed NL3 can then be concentrated and purified by any selected method.

[0231] Epitope-tagged NL3 may also be expressed in host CHO cells. NL3 may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged NL3 insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged FLS139, NL2 and NL3 can then be concentrated and purified by any selected method, such as by Ni²⁺-chelate affinity chromatography.

[0232] Glycosylated forms of NL3 were indeed expressed in CHO cells in poly-His tagged forms. Following PCR amplification, the NL3 DNA was subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used for the expression of NL3 in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24: 9 (1774-1779) (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

[0233] Twelve micrograms of NL3-encoding plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Quiagen), Dosper® or Eugene® (Boehringer Mannheim). The cells were grown and described in Lucas et al., supra. Approximately 3 x 10⁷ cells were frozen in an ampoule for further growth and production as described below.

[0234] The ampoule containing NL3 plasmid DNA was thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of medium and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective medium (0.2 µm filtered PS20 with 5% 0.2 µm diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective medium. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with 3 x 10⁵ cells/mL. The was exchanged with fresh medium by centrifugation and resuspension in production medium. Any suitable CHO medium may be employed, e.g., such as is described in U.S.P. 5,122,469, issued June 16, 1992. A 3L production spinner is seeded at 1.2 x 10⁶ cells/mL. On day 0, the cell number and pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L-glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane

emulsion, Dow Coming 365 Medical Grade Emulsion) were added. Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugation and filtered through a 0.22 μm filter. The filtrate was either stored at 4°C until loading onto a purification column.

[0235] The poly-His tagged were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned medium to a concentration of 5 mM. The conditioned medium was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4.5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

[0236] The homogeneity of the purified proteins was confirmed by SDS PEG and N-terminal amino acid sequencing performed by Edman degradation.

Example 5

Expression of NL3 in yeast

[0237] First, yeast expression vectors are constructed for intracellular production or secretion of

[0238] NL3 from the ADH2/GAPDH promoter. DNA encoding NL3, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of NL3. For secretion, DNA encoding NL3 can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of NL3.

[0239] Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

[0240] Recombinant NL3 can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing NL3 may further be purified using selected column chromatography resins.

Example 6

Expression of NL3 in Baculovirus transfected Insect Cells

[0241] The following method describes recombinant expression of NL3 in Baculovirus transfected insect cells.

[0242] The NL3 is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the NL3 or the desired portion of the NL3 (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

[0243] Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., *Baculovirus expression vectors: A laboratory Manual*, Oxford: Oxford University Press (1994).

[0244] Expressed poly-his tagged NL3 can then be purified, for example, by Ni^{2+} -chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362: 175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl_2 ; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni^{2+} -NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A_{280} with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A_{280} baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions

are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged NL3 are pooled and dialyzed against loading buffer. [0245] Alternatively, purification of the IgG tagged (or Fc tagged) FLS139, NL2 and NL3 can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Example 7

Preparation of Antibodies that bind NL3

[0246] This example illustrates preparation of monoclonal antibodies which can specifically bind NL3.

[0247] Techniques for producing the monoclonal antibodies are known in the art and are described, for example, in Coding, supra. Immunogens that may be employed include purified ligand homologues of the present invention, fusion proteins containing such ligand homologues, and cells expressing recombinant ligand homologues on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

[0248] Mice, such as Balb/c, are immunized with the immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice might also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing ELISA assays to detect the antibodies.

[0249] After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of the given ligand. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

[0250] The hybridoma cells will be screened in an ELISA for reactivity against the antigen. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the TIE ligand homologues herein is well within the skill in the art.

[0251] The positive hybridoma cells can be injected intraperitoneal into syngeneic Balb/c mice to produce ascites containing the anti- TIE-ligand monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 8

Induction of Endothelial Cell Apoptosis

[0252] The ability of the NL3 to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems), using a 96-well format, in 0% serum medium supplemented with 100 ng/ml VEGF. (As HUVEC cells are easily dislodged from the planting surface, all pipetting in the wells must be done as gently as practicable.)

[0253] The medium was aspirated and the cells washed once with PBS. 5 ml of 1 x trypsin was added to the cells in a T-175 flask, and the cells were allowed to stand until they were released from the plate (about 5-10 minutes). Trypsinization was stopped by adding 5 ml of growth media. The cells were spun at 1000 rpm for 5 minutes at 4°C. The medium was aspirated and the cells were resuspended in 10 ml of 10% serum complemented medium (Cell Systems), 1 x pen/strep.

[0254] The cells were plated on 96-well microtiterplates (Amersham Life Science, cytostar-T scintillating microplate, RPNQ160, sterile, tissue-culture treated, individually wrapped), in 10% serum (CSG-medium, Cell Systems), at a density of 2×10^4 cells per well in a total volume of 100 μ l. The NL5 and NL8 polypeptides were added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only as a negative control. As a positive control 1:3 serial dilutions of 50 μ l of a 3x stock of staurosporine were used. The ability of the NL5 polypeptide to induce apoptosis was determined using Annexin V, a member of the calcium and phospholipid binding proteins, to detect apoptosis.

[0255] 0.2 ml Annexin V - Biotin stock solution (100 μ g/ml) were diluted in 4.6 ml 2 x Ca²⁺ binding buffer and 2.5% BSA (1:25 dilution). 50 μ l of the diluted Annexin V - Biotin solution were added to each well (except controls) to a final concentration of 1.0 μ g/ml. The samples were incubated for 10-15 minutes with Annexin-Biotin prior to direct addition of ³⁵S-Streptavidin. ³⁵S-Streptavidin was diluted in 2x Ca²⁺ Binding buffer, 2.5% BSA and was added to all wells at a

final concentration of 3×10^4 cpm/well. The plates were then sealed, centrifuged at 1000 rpm for 15 minutes and placed on orbital shaker for 2 hours. The analysis was performed on 1450 Microbeta Trilux (Wallac).

[0256] were positive in this assay. This result further confirms the potential utility of these, and potentially related, molecules in cancer therapy.

Deposit of Material

[0257] As noted before, the following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

Material	ATCC Dep. No.	Deposit Date
NL2-DNA 22780-1078	209284	9/18/97
NL3-DNA 33457-1078	209283	9/18/97
FLS139-DNA16451-1078	209281	9/18/97

[0258] These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of the deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC §122 and Commissioner's rules pursuant thereto (including 37 C.F.R. § 1.14 with particular reference to 886 OG 683).

[0259] The assignee of the present application has agreed that if a culture of the material on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

[0260] The present specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of the invention. The deposit of material herein does not constitute an admission that the written description is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

SEQUENCE LISTING

[0261]

(1) GENERAL INFORMATION:

(i) APPLICANT: Genentech, Inc.

(ii) TITLE OF INVENTION: Tie Receptor Tyrosine Kinase Ligand Homologues

(iii) NUMBER OF SEQUENCES: 17

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1869 base pairs

(S) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

EP 1 482 040 B1

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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10

15

20

25

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EP 1 482 040 B1

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EP 1 482 040 B1

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 ATGGCGGACT CAGTCACATT GACTGACGGG GACCAGGGCT TGTGTGGGTC 1750
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 ACAAGCAGGC GCCAATGGTA TCTGGGCGGA GCTCACAGAG TTCTTGGAAT 1850
 AAAAGCAACC TCAGAACAC 1869

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 406 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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 50 55 60
 Arg Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala
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 80 85 90
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 55 Pro Glu Met Ala Gln Pro Val Asp Pro Ala His Asn Val Ser Arg
 170 175 180

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	Pro Phe Leu Val Asn Cys Lys Met Thr Ser Xaa Gly Gly Trp Thr	
	215	220 225
10	Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro	
	230	235 240
	Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe	
	245	250 255
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	275	280 285
20	Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr	
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25	Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp	
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	Gln Asp His Asn Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu	
	335	340 345
30	Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn	
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	Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys	
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35	Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu	
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40	Ser	
	406	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

EP 1 482 040 B1

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 ACTGCAGGGG ATTCCCTGAG CCTCCACAGT GGGAGGCCCT TTACCACCTA 700
 25 TGACGCTGAC CACGATTCAA GCAACAGCAA CTGTGCAGTG ATTGTCCACG 750
 GTGCTGGTG GTATGCATCC TGTTACCGAT CAAATCTCAA TGGTCGCTAT 800
 GCAGTGTCTG AGGCTGCCGC CCACAAATAT GGCATTGACT GGGCTCAGG 850
 30 CCGTGGTGTG GGCCACCCCT ACCGCAGGGT TCGGATGATG CTTGATAGG 900
 GCACTCTGGC AGCCAGTGCC CTTATCTCTC CTGTACAGCT TCCGGATCGT 950
 CAGCCACCTT GCCTTTGCCA ACCACCTCTG CTTGCCTGTC CACATTTAAA 1000
 35 AATAAAATCA TTTTAGCCCT TTCA 1024

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu Leu
 1 5 10 15
 Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro
 20 25 30
 Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser

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				35					40					45				
				Cys	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Gly	Glu	Lys	Gly	Ala	Pro	Gly
				50					55								60	
5				Pro	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Lys	Met	Gly	Pro	Lys	Gly
				65					70								75	
				Glu	Pro	Gly	Pro	Arg	Asn	Cys	Arg	Glu	Leu	Leu	Ser	Gln	Gly	Ala
				80					85								90	
10				Thr	Leu	Ser	Gly	Trp	Tyr	His	Leu	Cys	Leu	Pro	Glu	Gly	Arg	Ala
				95					100								105	
				Leu	Pro	Val	Phe	Cys	Asp	Met	Asp	Thr	Glu	Gly	Gly	Gly	Trp	Leu
				110					115								120	
15				Val	Phe	Gln	Arg	Arg	Gln	Asp	Gly	Ser	Val	Asp	Phe	Phe	Arg	Ser
				125					130								135	
				Trp	Ser	Ser	Tyr	Arg	Ala	Gly	Phe	Gly	Asn	Gln	Glu	Ser	Glu	Phe
				140					145								150	
20				Trp	Leu	Gly	Asn	Glu	Asn	Leu	His	Gln	Leu	Thr	Leu	Gln	Gly	Asn
				155					160								165	
				Trp	Glu	Leu	Arg	Val	Glu	Leu	Glu	Asp	Phe	Asn	Gly	Asn	Arg	Thr
				170					175								180	
25				Phe	Ala	His	Tyr	Ala	Thr	Phe	Arg	Leu	Leu	Gly	Glu	Val	Asp	His
				185					190								195	
				Tyr	Gln	Leu	Ala	Leu	Gly	Lys	Phe	Ser	Glu	Gly	Thr	Ala	Gly	Asp
				200					205								210	
30				Ser	Leu	Ser	Leu	His	Ser	Gly	Arg	Pro	Phe	Thr	Thr	Tyr	Asp	Ala
				215					220								225	
				Asp	His	Asp	Ser	Ser	Asn	Ser	Asn	Cys	Ala	Val	Ile	Val	His	Gly
				230					235								240	
35				Ala	Trp	Trp	Tyr	Ala	Ser	Cys	Tyr	Arg	Ser	Asn	Leu	Asn	Gly	Arg
				245					250								255	
				Tyr	Ala	Val	Ser	Glu	Ala	Ala	Ala	His	Lys	Tyr	Gly	Ile	Asp	Trp
				260					265								270	
40				Ala	Ser	Gly	Arg	Gly	Val	Gly	His	Pro	Tyr	Arg	Arg	Val	Arg	Met
				275					280								285	
				Met	Leu	Arg												
				288														

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
 GCTCCTTCTT TTTATTGTTT CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
 5 ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTGCT 150
 ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
 TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
 10 TTCAAAAAC TCAACATATTT GATCAGTCTT TTTATGATCT ATCGTGCA 300
 ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
 ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACCT GAACTCAACT 400
 15 CAAAACCTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
 AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
 TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
 20 ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
 TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
 GACTAGTATT CAAGAACCCA CAGAAATTTT TCTATCTTCC AAGCCAAGAG 700
 25 CACCAAGAAC TACTCCCTTT CTTCACTTGA ATGAAATAAG AAATGTAAAA 750
 CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
 TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850
 30 TCTACTGTGA TGTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
 ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
 TTTTGGGAGG CTTGATGGAG AATTTTGTTT GGGCCTAGAG AAGATATACT 1000
 35 CCATAGTGAA GCAATCTAAT TATGTTTAC GAATTGAGTT GGAAGACTGG 1050
 AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100
 AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150
 40 CAATCCCGGA AAACAAAGAT TTGGTGT TTTTCTTGGG TCACAAAGCA 1200
 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250
 45 TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

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 5 GGAAGGTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400
 TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450
 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500
 10 AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550
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 15 CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700
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 20 TAAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850
 TAAATGTTGT AGTATTAATT TCAAACTAA AAATCGTCAG CACAGAGTAT 1900
 GTGTAAAAAT CTGTAATACA AATTTTTTAAA CTGATGCTTC ATTTTGCTAC 1950
 25 AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000
 AAGCAGAATT AAATACTGTA TTAAATAAG TTCGCTGTCT TT 2042

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

40	Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile	1	5	10	15
	Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser	20	25	30	
45	Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile	35	40	45	
	Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe	50	55	60	
50	Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu	65	70	75	
	Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser	80	85	90	
55	Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys				

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	95	100	105
5	Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu 110 115 120		
	Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln 125 130 135		
10	Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln 140 145 150		
	Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys 155 160 165		
15	Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln 170 175 180		
	Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln 185 190 195		
20	Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu 200 205 210		
	Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr 215 220 225		
25	Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp 230 235 240		
	Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His 245 250 255		
30	Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe 260 265 270		
	His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile 275 280 285		
35	Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu 290 295 300		
	Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu 305 310 315		
40	Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val 320 325 330		
	Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile 335 340 345		
45	Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu 350 355 360		
	His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu 365 370 375		
50	Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly 380 385 390		
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(2) INFORMATION FOR SEQ ID NO:7:

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
TGGTTGGCAA AGGCAAGGTG GCTGACGATC CGG 33

(2) INFORMATION FOR SEQ. ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GTGGCCCTTA TCTCTCCTGT ACAGCTTCCG GATCGTCAGC CAC 43

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
TCCATTCCCA CCTATGACGC TGACCCA 27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
CCACGTTGGC TTGAAATTGA 20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
CCTCCAGAAT TGATCAAGAC AATTCATGAT TTGATTCTCT ATCTCCAGAG 50

(2) INFORMATIONFOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
TCGTCTAACA TAGCAAATC 19

(2) INFORMATION FOR SEQ ID NO:16:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
TTCATAATACG ACTCACTATA GGGCAAGTTG TCCTCC 36

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID. NO:17:
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5 tgtcagggaa ccgaggggtc caccgacctc ccgttagccc ctgagagccg 450
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 15 cgctgcacc ggtgcccag ggattgccag gagctgttcc aggttgggga 750
 gaggcagagt ggactatttg aaatccagcc tcaggggtct ccgccatttt 800
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Ala	Thr	Ala	Val	Leu	Leu	Ser	Ala	Gln	Gly	Gly	Pro	Val	Gln	Ser
				20					25					30
Lys	Ser	Pro	Arg	Phe	Ala	Ser	Trp	Asp	Glu	Met	Asn	Val	Leu	Ala
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His	Gly	Leu	Leu	Gln	Leu	Gly	Gln	Gly	Leu	Arg	Glu	His	Ala	Glu
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Arg	Thr	Arg	Ser	Gln	Leu	Ser	Ala	Leu	Glu	Arg	Arg	Leu	Ser	Ala
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Cys	Gly	Ser	Ala	Cys	Gln	Gly	Thr	Glu	Gly	Ser	Thr	Asp	Leu	Pro
				80					85					90
Leu	Ala	Pro	Glu	Ser	Arg	Val	Asp	Pro	Glu	Val	Leu	His	Ser	Leu
				95					100					105

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	110	115	120
5	His Lys Val Ala Gln Gln Gln Arg His Leu Glu Lys Gln His Leu		
	125	130	135
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	Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly		
20	185	190	195
	Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro		
	200	205	210
25	Pro Phe Leu Val Asn Cys Lys Met Thr Ser Xaa Gly Gly Trp Thr		
	215	220	225
	Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro		
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	Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe		
	245	250	255
35	Trp Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn		
	260	265	270
	Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu		
40	275	280	285
	Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr		
45	290	295	300
	Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr		
	305	310	315
50	Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp		
	320	325	330

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	Gln Asp His Asn Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu	
	335	340 345
5	Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn	
	350	355 360
10	Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys	
	365	370 375
15	Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu	
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35	ccaggaacac ccagctgcc caggaccag ggaactggaa gccagcaaag 150
	ttgtcctcct gccagttgt cccggagctc caggaagtcc tggggagaag 200
40	ggagccccag gtcctcaagg gccacctgga ccaccaggca agatggggcc 250
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          20           25           30
Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser
          35           40           45
Cys Pro Gly Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly
          50           55           60
Pro Gln Gly Pro Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly
          65           70           75
Glu Pro Gly Pro Arg Asn Cys Arg Glu Leu Leu Ser Gln Gly Ala
          80           85           90
Thr Leu Ser Gly Trp Tyr His Leu Cys Leu Pro Glu Gly Arg Ala
          95          100          105

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					110					115					120
5	Val	Phe	Gln	Arg	Arg	Gln	Asp	Gly	Ser	Val	Asp	Phe	Phe	Arg	Ser
					125					130					135
	Trp	Ser	Ser	Tyr	Arg	Ala	Gly	Phe	Gly	Asn	Gln	Glu	Ser	Glu	Phe
10					140					145					150
	Trp	Leu	Gly	Asn	Glu	Asn	Leu	His	Gln	Leu	Thr	Leu	Gln	Gly	Asn
					155					160					165
15	Trp	Glu	Leu	Arg	Val	Glu	Leu	Glu	Asp	Phe	Asn	Gly	Asn	Arg	Thr
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	Phe	Ala	His	Tyr	Ala	Thr	Phe	Arg	Leu	Leu	Gly	Glu	Val	Asp	His
20					185					190					195
	Tyr	Gln	Leu	Ala	Leu	Gly	Lys	Phe	Ser	Glu	Gly	Thr	Ala	Gly	Asp
					200					205					210
25	Ser	Leu	Ser	Leu	His	Ser	Gly	Arg	Pro	Phe	Thr	Thr	Tyr	Asp	Ala
					215					220					225
	Asp	His	Asp	Ser	Ser	Asn	Ser	Asn	Cys	Ala	Val	Ile	Val	His	Gly
30					230					235					240
	Ala	Trp	Trp	Tyr	Ala	Ser	Cys	Tyr	Arg	Ser	Asn	Leu	Asn	Gly	Arg
					245					250					255
35	Tyr	Ala	Val	Ser	Glu	Ala	Ala	Ala	His	Lys	Tyr	Gly	Ile	Asp	Trp
					260					265					270
	Ala	Ser	Gly	Arg	Gly	Val	Gly	His	Pro	Tyr	Arg	Arg	Val	Arg	Met
40					275					280					285
	Met	Leu	Arg												
45															

<210> 5

<211> 2042

<212> DNA

50 <213> Homo sapiens

<400> 5

55 gcggacgcgt gggtgaaatt gaaaatcaag ataaaaatgt tcacaattaa 50

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 5 acaattcatc atttgattct ctatctccag agccaaaatc aagatttgct 150
 atggttagacg atgtaaaaat tttagccaat ggcctccttc agttgggaca 200
 10 tgggtcttaaa gactttgtcc ataagacgaa gggccaaatt aatgacatat 250
 ttcaaaaact caacatattt gatcagttct tttatgatct atcgctgcaa 300
 15 accagtgaag tcaaagaaga agaaaaggaa ctgagaagaa ctacatataa 350
 actacaagtc aaaaatgaag aggtaaagaa tatgtcactt gaactcaact 400
 caaaacttga aagcctccta gaagaaaaaa ttctacttca acaaaaagtg 450
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 tccagaacac ccagaagtaa cttcacttaa aacttttgta gaaaaacaag 550
 25 ataatagcat caaagacctt ctccagaccg tggaagacca atataaaca 600
 ttaaaccaac agcatagtca aataaaagaa atagaaaatc agctcagaag 650
 30 gactagtatt caagaacca cagaaatttc tctatcttcc aagccaagag 700
 caccaagaac tactcccttt cttcagttga atgaaataag aaatgtaaaa 750
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 atagatggat cacaaaactt caatgaaacg tgggagaact acaaatatgg 950
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 caaaatctaa gccagagagg agaagaggat tatcttggaa gtctcaaaat 1350
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 ttcagaaagc tttgaatgaa ctgaggcaat ttaaaggcat atttaaccat 1450
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 15 agaaagcttg agaaatagat tttttttatc ttaaagtcac tgtctattta 1550
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 20 aatcaaaatt cttataatac tatttgtttt aaattttgtg atgtgggaat 1650
 caattttaga tggtcacaat ctagattata atcaataggt gaacttatta 1700
 25 aataactttt ctaaataaaa aatttagaga cttttatttt aaaaggcatc 1750
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 30 taaaactcta aacttgacta aatacagagg actggtaatt gtacagttct 1850
 taaagtgtgt agtattaatt tcaaaactaa aaatcgtcag cacagagtat 1900
 35 gtgtaaaaat ctgtaataca aattttttaa ctgatgcttc attttgctac 1950
 aaaataattt ggagtaaag tttgatatga tttatttatg aaacctaag 2000
 40 aagcagaatt aaatactgta ttaaaataag ttcgctgtct tt 2042

<210> 6
 <211> 460
 <212> PRT
 45 <213> Homo sapiens

 <400> 6

50 Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile
 1 5 10 15

 Ser Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser
 55 20 25 30

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	Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile	
					35					40					45	
5	Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe	
					50					55					60	
10	Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu	
					65					70					75	
15	Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser	
					80					85					90	
20	Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys	
					95					100					105	
25	Leu	Gln	Val	Lys	Asn	Glu	Glu	Val	Lys	Asn	Met	Ser	Leu	Glu	Leu	
					110					115					120	
30	Asn	Ser	Lys	Leu	Glu	Ser	Leu	Leu	Glu	Glu	Lys	Ile	Leu	Leu	Gln	
					125					130					135	
35	Gln	Lys	Val	Lys	Tyr	Leu	Glu	Glu	Gln	Leu	Thr	Asn	Leu	Ile	Gln	
					140					145					150	
40	Asn	Gln	Pro	Glu	Thr	Pro	Glu	His	Pro	Glu	Val	Thr	Ser	Leu	Lys	
					155					160					165	
45	Thr	Phe	Val	Glu	Lys	Gln	Asp	Asn	Ser	Ile	Lys	Asp	Leu	Leu	Gln	
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50	Thr	Val	Glu	Asp	Gln	Tyr	Lys	Gln	Leu	Asn	Gln	Gln	His	Ser	Gln	
					185					190					195	
55	Ile	Lys	Glu	Ile	Glu	Asn	Gln	Leu	Arg	Arg	Thr	Ser	Ile	Gln	Glu	
					200					205					210	
	Pro	Thr	Glu	Ile	Ser	Leu	Ser	Ser	Lys	Pro	Arg	Ala	Pro	Arg	Thr	
					215					220					225	
	Thr	Pro	Phe	Leu	Gln	Leu	Asn	Glu	Ile	Arg	Asn	Val	Lys	His	Asp	
					230					235					240	
	Gly	Ile	Pro	Ala	Glu	Cys	Thr	Thr	Ile	Tyr	Asn	Arg	Gly	Glu	His	
					245					250					255	

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	Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe		
	260	265	270
5	His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile		
	275	280	285
	Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu		
10	290	295	300
	Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu		
	305	310	315
15	Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val		
	320	325	330
	Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile		
20	335	340	345
	Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu		
	350	355	360
25	His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu		
	365	370	375
	Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly		
30	380	385	390
	His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp His		
35	395	400	405
	Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro		
	410	415	420
40	Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys		
	425	430	435
	Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu		
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<210> 7

<211> 33

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<213> Artificial Sequence

<220>

<221> source

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<223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

<400> 7

atgagggtggc caagcctgcc cgaagaaaga ggc 33

<210> 8

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<213> Artificial Sequence

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<221> source

<223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

<400> 8

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<211> 24

<212> DNA

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<223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

<400> 9

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<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

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<221> source

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<400> 10

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<223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

<400> 11

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<212> DNA

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<220>
<221> source
<223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

5 <400> 12
tccattccca cctatgacgc tgaccca 27

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20 <400> 13
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 <223> /note= "Description of Artificial sequence: Synthetic oligonucleotide probe"

35 <400> 14
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 <213> Artificial Sequence

45 <220>
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50 <400> 15
tcgtctaaca tagcaaadc 19

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60 <220>
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65 <400> 16
ttctaatacg actcactata gggcaagttg tcctcc 36

70 <210> 17
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<213> Artificial Sequence

<220>

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<400> 17

tgaaattaac cctcactaaa gggacgtggt cagcgt 36

10 SEQUENCE LISTING

[0263]

(1) GENERAL INFORMATION:

15

(i) APPLICANT: Genentech, Inc.

(ii) TITLE OF INVENTION : Tie Receptor Tyrosine Kinase Ligand Homologues

20

(iii) NUMBER OF SEQUENCES: 17

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 1869 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35

GCCGAGCTGA GCGGATCCTC ACATGACTGT GATCCGATTC TTTCCAGCGG 50

CTTCTGCAAC CAAGCGGGTC TTACCCCCGG TCCTCCGCGT CTCCAGTCCT 100

40

45

50

55

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CGCACCTGGA ACCCCAACGT CCCCAGAGAGT CCCCGAATCC CCGCTCCCAG 150
 5 GCTACCTAAG AGGATGAGCG GTGCTCCGAC GGCCGGGGCA GCCCTGATGC 200
 TCTGCGCCGC CACCGCCGTG CTA CTGAGCG CTCAGGGCGG ACCCGTGAG 250
 TCCAAGTCGC CGCGCTTTGC GTCCTGGGAC GAGATGAATG TCCTGGCGCA 300
 10 CGGACTCCTG CAGCTCGGCC AGGGGCTGCG CGAACACGCG GAGCGCACCC 350
 GCAGTCAGCT GAGCGCGCTG GAGCGGCGCC TGAGCGCGTG CGGGTCCGCC 400
 TGTCAGGGAA CCGAGGGGTC CACCGACCTC CCGTTAGCCC CTGAGAGCCG 450
 15 GGTGGACCCT GAGGTCCTTC ACAGCCTGCA GACACAATC AAGGCTCAGA 500
 ACAGCAGGAT CCAGCAATC TTCCACAAGG TGGCCAGCA GCAGCGGCAC 550
 CTGGAGAAGC AGCACCTGCG AATTCAGCAT CTGCAAAGCC AGTTTGGCCT 600
 20 CCTGGACCAC AAGCACCTAG ACCATGAGGT GGCCAAGCCT GCCCGAAGAA 650
 AGAGGCTGCC CGAGATGGCC CAGCCAGTTG ACCCGGCTCA CAATGTCAGC 700
 25 CGCCTGCACC GGCTGCCCAG GGATTGCCAG GAGCTGTTCC AGGTTGGGGA 750
 GAGGCAGAGT GGACTATTTG AAATCCAGCC TCAGGGGTCT CCGCCATTTT 800
 TGGTGAATG CAAGATGACC TCAGATGGAG GCTGGACAGT AATTCAGAGG 850
 30 CGCCACGATG GCTCAGTGGA CTTCAACCGG CCCTGGGAAG CCTACAAGGC 900
 GGGGTTTGGG GATCCCCACG GCGAGTTCTG GCTGGGTCTG GAGAAGGTGC 950
 ATAGCATCAC GGGGGACCGC AACAGCCGCC TGGCCGTGCA GCTGCGGGAC 1000
 35 TGGGATGGCA ACGCCGAGTT GCTGCAGTTC TCCGTGCACC TGGGTGGCGA 1050
 GGACACGGCC TATAGCCTGC AGCTCACTGC ACCCGTGGCC GGCCAGCTGG 1100
 40 GCGCCACCAC CGTCCCACCC AGCGGCCTCT CCGTACCCTT CTCCACTTGG 1150
 GACCAGGATC ACGACCTCCG CAGGGACAAG AACTGCGCCA AGAGCCTCTC 1200
 TGGAGGCTGG TGGTTTGGCA CCTGCAGCCA TTCCAACCTC AACGGCCAGT 1250
 45 ACTTCCGCTC CATCCCACAG CAGCGGCAGA AGCTTAAGAA GGAATCTTC 1300
 TGGAAGACCT GGCGGGGCGG CTA CTACCCG CTGCAGGCCA CCACCATGTT 1350
 GATCCAGCCC ATGGCAGCAG AGGCAGCCTC CTAGCGTCCT GGCTGGGCCT 1400
 50 GGTCCCAGGC CCACGAAAGA CGGTGACTCT TGGCTCTGCC CGAGGATGTG 1450
 GCCGTTCCT GCCTGGGCAG GGGCTCCAAG GAGGGGCCAT CTGGAACTT 1500
 55 GTGGACAGAG AAGAAGACCA CGACTGGAGA AGCCCCCTT CTGAGTGAG 1550

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GGGGGCTGCA TGC GTTGCCT CCTGAGATCG AGGCTGCAGG ATATGCTCAG 1600
ACTCTAGAGG CGTGGACCAA GGGGCATGGA GCTTCACTCC TTGCTGGCCA 1650
GGGAGTTGGG GACTCAGAGG GACCACTTGG GGCCAGCCAG ACTGGCCTCA 1700
ATGGCGGACT CAGTCACATT GACTGACGGG GACCAGGGCT TGTGTGGGTC 1750
GAGAGCGCCC TCATGGTGCT GGTGCTGTTG TGTGTAGGTC CCCTGGGGAC 1800
ACAAGCAGGC GCCAATGGTA TCTGGGCGGA GCTCACAGAG TTCTTGGAAT 1850
AAAAGCAACC TCAGAACAC 1869

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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	Met Ser Gly Ala Pro Thr Ala Gly Ala Ala Leu Met Leu Cys Ala	
	1 5 10 15	
5	Ala Thr Ala Val Leu Leu Ser Ala Gln Gly Gly Pro Val Gln Ser	
	20 25 30	
	Lys Ser Pro Arg Phe Ala Ser Trp Asp Glu Met Asn Val Leu Ala	
	35 40 45	
10	His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu	
	50 55 60	
	Arg Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala	
	65 70 75	
15	Cys Gly Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro	
	80 85 90	
	Leu Ala Pro Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu	
	95 100 105	
20	Gln Thr Gln Leu Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe	
	110 115 120	
	His Lys Val Ala Gln Gln Gln Arg His Leu Glu Lys Gln His Leu	
	125 130 135	
25	Arg Ile Gln His Leu Gln Ser Gln Phe Gly Leu Leu Asp His Lys	
	140 145 150	
	His Leu Asp His Glu Val Ala Lys Pro Ala Arg Arg Lys Arg Leu	
	155 160 165	
30	Pro Glu Met Ala Gln Pro Val Asp Pro Ala His Asn Val Ser Arg	
	170 175 180	
35		
40		
45		
50		
55		

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	Leu His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly	
	185	190 195
5	Glu Arg Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro	
	200	205 210
	Pro Phe Leu Val Asn Cys Lys Met Thr Ser Xaa Gly Gly Trp Thr	
	215	220 225
10	Val Ile Gln Arg Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro	
	230	235 240
	Trp Glu Ala Tyr Lys Ala Gly Phe Gly Asp Pro His Gly Glu Phe	
15	245	250 255
	Trp Leu Gly Leu Glu Lys Val His Ser Ile Thr Gly Asp Arg Asn	
	260	265 270
	Ser Arg Leu Ala Val Gln Leu Arg Asp Trp Asp Gly Asn Ala Glu	
20	275	280 285
	Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu Asp Thr Ala Tyr	
	290	295 300
	Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu Gly Ala Thr	
25	305	310 315
	Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr Trp Asp	
	320	325 330
	Gln Asp His Asn Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser Leu	
30	335	340 345
	Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn	
	350	355 360
	Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys	
35	365	370 375
	Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu	
	380	385 390
40	Gln Ala Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala	
	395	400 405
	Ser	
45	406	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CGGACGCGTG GGCCCCTGGT GGGCCCAGCA AGATGGATCT ACTGTGGATC 50
 CTGCCCTCCC TGTGGCTTCT CCTGCTTGGG GGGCCTGCCT GCCTGAAGAC 100
 5 CCAGGAACAC CCCAGCTGCC CAGGACCCAG GGAAGTGGAA GCCAGCAAAG 150
 TTGTCCTCCT GCCCAGTTGT CCCGGAGCTC CAGGAAGTCC TGGGGAGAAG 200
 10 GGAGCCCCAG GTCCTCAAGG GCCACCTGGA CCACCAGGCA AGATGGGCCC 250
 CAAGGGTGAG CCAGGCCCCA GAAACTGCCG GGAGCTGTTG AGCCAGGGCG 300
 CCACCTTGAG CGGCTGGTAC CATCTGTGCC TACCTGAGGG CAGGGCCCTC 350
 15 CCAGTCTTTT GTGACATGGA CACCGAGGGG GCGGCTGGC TGGTGTTC 400
 GAGGCGCCAG GATGGTTCTG TGGATTTCTT CCGCTCTTGG TCCTCCTACA 450
 GAGCAGGTTT TGGGAACCAA GAGTCTGAAT TCTGGCTGGG AAATGAGAAT 500
 20 TTGCACCAGC TTAATCTCCA GGGTAACTGG GAGCTGCGGG TAGAGCTGGA 550
 AGACTTTAAT GGTAACCGTA CTTTCGCCCA CTATGCGACC TTCCGCCTCC 600
 TCGGTGAGGT AGACCACTAC CAGCTGGCAC TGGGCAAGTT CTCAGAGGGC 650
 25 ACTGCAGGGG ATTCCCTGAG CCTCCACAGT GGGAGGCCCT TTACCACCTA 700
 TGACGCTGAC CACGATTCAA GCAACAGCAA CTGTGCAGTG ATTGTCCACG 750
 GTGCCTGGTG GTATGCATCC TGTTACCGAT CAAATCTCAA TGGTCGCTAT 800
 30 GCAGTGTCTG AGGCTGCCGC CCACAAATAT GGCATTGACT GGGCCTCAGG 850
 CCGTGGTGTG GGCCACCCCT ACCGCAGGGT TCGGATGATG CTTTCGATAGG 900
 35 GCACTCTGGC AGCCAGTGCC CTTATCTCTC CTGTACAGCT TCCGGATCGT 950
 CAGCCACCTT GCCTTTGCCA ACCACCTCTG CTTGCCTGTC CACATTTAAA 1000
 AATAAAATCA TTTTAGCCCT TTCA 1024

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu Leu
 1 5 10 15
 Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro
 20 25 30
 Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser

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	35	40	45
5	Cys Pro Gly Ala	Pro Gly Ser Pro Gly Glu Lys Gly Ala	Pro Gly
	50	55	60
	Pro Gln Gly Pro	Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly	
	65	70	75
10	Glu Pro Gly Pro	Arg Asn Cys Arg Glu Leu Leu Ser Gln Gly Ala	
	80	85	90
	Thr Leu Ser Gly	Trp Tyr His Leu Cys Leu Pro Glu Gly Arg Ala	
	95	100	105
15	Leu Pro Val Phe	Cys Asp Met Asp Thr Glu Gly Gly Gly Trp Leu	
	110	115	120
	Val Phe Gln Arg	Arg Gln Asp Gly Ser Val Asp Phe Phe Arg Ser	
	125	130	135
20	Trp Ser Ser Tyr	Arg Ala Gly Phe Gly Asn Gln Glu Ser Glu Phe	
	140	145	150
	Trp Leu Gly Asn	Glu Asn Leu His Gln Leu Thr Leu Gln Gly Asn	
	155	160	165
25	Trp Glu Leu Arg	Val Glu Leu Glu Asp Phe Asn Gly Asn Arg Thr	
	170	175	180
	Phe Ala His Tyr	Ala Thr Phe Arg Leu Leu Gly Glu Val Asp His	
	185	190	195
30	Tyr Gln Leu Ala	Leu Gly Lys Phe Ser Glu Gly Thr Ala Gly Asp	
	200	205	210
	Ser Leu Ser Leu	His Ser Gly Arg Pro Phe Thr Thr Tyr Asp Ala	
	215	220	225
	Asp His Asp Ser	Ser Asn Ser Asn Cys Ala Val Ile Val His Gly	
	230	235	240
40	Ala Trp Trp Tyr	Ala Ser Cys Tyr Arg Ser Asn Leu Asn Gly Arg	
	245	250	255
	Tyr Ala Val Ser	Glu Ala Ala Ala His Lys Tyr Gly Ile Asp Trp	
	260	265	270
45	Ala Ser Gly Arg	Gly Val Gly His Pro Tyr Arg Arg Val Arg Met	
	275	280	285
	Met Leu Arg		
	288		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2042 base pairs
- (B) TYPE: Nuclei Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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      GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
      ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150
10     ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
      TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
      TTCAAAACT CAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
15     ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
      ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
      CAAAACCTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
20     AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
      TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
      ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
25     TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
      GACTAGTATT CAAGAACCCA CAGAAATTTC TCTATCTTCC AAGCCAAGAG 700
30     CACCAAGAAC TACTCCCTTT CTTCACTTGA ATGAAATAAG AAATGTAAAA 750
      CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
      TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850
35     TCTACTGTGA TGTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
      ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
      TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
40     CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050
      AAAGACAACA AACATTATAT TGAATATTCT TTTACTTGG GAAATCACGA 1100
      AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150
45     CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTAAGTGGGA TCACAAAGCA 1200
      AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250
50     TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

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CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTCAAAAT 1350
 5 GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400
 TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450
 TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500
 10 AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550
 AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600
 AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650
 15 CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700
 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750
 ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAAACTA GTACTCTTGT 1800
 TAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850
 TAAATGTTGT AGTATTAATT TCAAACTAA AAATCGTCAG CACAGAGTAT 1900
 20 GTGTAAAAAT CTGTAATACA AATTTTAAA CTGATGCTTC ATTTTGCTAC 1950
 AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000
 AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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	Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile
	1				5					10					15
5	Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser
					20					25					30
	Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile
					35					40					45
10	Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe
					50					55					60
	Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu
					65					70					75
15	Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser
					80					85					90
	Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys
20															
25															
30															
35															
40															
45															
50															
55															

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	95	100	105
5	Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met Ser Leu Glu Leu 110	115	120
	Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile Leu Leu Gln 125	130	135
10	Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu Ile Gln 140	145	150
	Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu Lys 155	160	165
15	Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln 170	175	180
	Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln 185	190	195
20	Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu 200	205	210
	Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr 215	220	225
25	Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp 230	235	240
	Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His 245	250	255
30	Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe 260	265	270
	His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile 275	280	285
35	Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu 290	295	300
40	Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu 305	310	315
	Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val 320	325	330
45	Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile 335	340	345
	Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu 350	355	360
50	His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu 365	370	375
	Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly 380	385	390

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(2) INFORMATION FOR SEQ ID NO:7:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
ATGAGGTGGC CAAGCCTGCC CGAAGAAAGA GGC 33

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(i) SEQUENCE CHARACTERISTICS:

- 35

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 45

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(2) INFORMATION FOR SEQ ID NO:10:

- 55

- (A) LENGTH: 33 base pairs

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- (B) TYPE: Nucleic Acid
- (C) STRN4DEDNESS: Single
- (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
TGGTTGGCAA AGGCAAGGTG GCTGACGATC CGG 33

10 TGGTTGGCAA AGGCAAGGTG GCTGACGATC CGG 33

(2) INFORMATION FOR SEQ ID NO:11:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
GTGGCCCTTA TCTCTCCTGT ACAGCTTCCG GATCGTCAGC CAC 43

25 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
TCCATTCCCA CCTATGACGC TGACCCA 27

35 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 20 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
CCACGTTGGC TTGAAATTGA 20

(2) INFORMATION FOR SEQ ID NO:14:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
CCTCCAGAAT TGATCAAGAC AATTCATGAT TTGATTCTCT ATCTCCAGAG 50

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 19 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
TCGTCTAACA TAGCAAATC 19

(2) INFORMATION FOR SEQ ID NO:16:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
20 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
TTCTAATACG ACTCACTATA GGGCAAGTTG TCCTCC 36

25 TTCTAATACG ACTCACTATA GGGCAAGTTG TCCTCC 36

(2) INFORMATION FOR SEQ ID NO:17:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
TGAAATTAAC CCTCACTAAA GGGACGTGGT CAGCGT 36

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Claims

1. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide having at least 90% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ.ID. NO: 4).
- 45 2. An isolated nucleic acid molecule according to claim 1 wherein the encoded polypeptide has at least 95% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
3. An isolated nucleic acid molecule according to claim 2 wherein the encoded polypeptide has at least 98% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
- 50 4. An isolated nucleic acid molecule according to claim 3 wherein the encoded polypeptide has at least 99% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
- 55 5. An isolated nucleic acid molecule according to claim 4, wherein the encoded polypeptide has the amino acid sequence of native human NL3 polypeptide(SEQ. ID.NO: 4).
6. The isolated nucleic acid molecule of claim 5 which comprises the coding region of SEQ.ID. NO: 3.

7. The isolated nucleic acid molecule of claim 1 which comprises the fibrinogen-like domain of SEQ. ID. NO: 3.
8. A vector which comprises a nucleic acid molecule of any one of claims 1 to 7.
- 5 9. A recombinant host cell transformed with a nucleic acid molecule according to any one of claims 1 to 7.
10. The recombinant host cell of claim 9 which is a prokaryotic cell.
11. The recombinant host cell of claim 9 which is a eukaryotic cell.
- 10 12. An isolated polypeptide, comprising an NL3 amino acid sequence having at least 90% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
- 15 13. An isolated polypeptide according to claim 12, comprising an NL3 amino acid sequence having at least 95% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
14. An isolated polypeptide according to claim 13, comprising an NL3 amino acid sequence having at least 98% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
- 20 15. An isolated polypeptide according to claim 14, comprising an NL3 amino acid sequence having at least 99% sequence identity with the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
- 25 16. An isolated polypeptide according to claim 15, comprising an NL3 amino acid sequence having the amino acid sequence of native human NL3 polypeptide(SEQ. ID. NO: 4).
17. An antibody which specifically binds the NL3 amino acid sequence of the polypeptide according to any one of claims 12 to 16.
- 30 18. The antibody of claim 17 which is a monoclonal antibody.
19. The antibody of claim 8 which has nonhuman complementarity determining region (CDR) residues and human framework (FR) residues.
20. The antibody of claim 17 which is labelled.
- 35 21. A composition comprising a polypeptide of any one of claims 12 to 16 in association with a carrier.
22. A composition comprising an antibody of claim 17 in association with a carrier.
- 40 23. The composition of claim 22 further comprising a second antibody or a cytotoxic or chemotherapeutic agent.
24. A conjugate comprising a polypeptide of any one of claims 12 to 16 or an antibody of claim 17, fused to a further therapeutic or cytotoxic agent.
- 45 25. The conjugate of claim 24 wherein the further therapeutic agent is a toxin, a different TIE ligand, or a member of the vascular endothelial growth factor (VEGF) family.
26. A polypeptide according to any one of claims 12 to 16, or an antibody according to claim 17, for use in a method of medical treatment.
- 50 27. Use of a polypeptide according to any one of claims 12 to 16 in the preparation of a medicament for the induction of endothelial cell apoptosis or inhibition of tumour growth.

Patentansprüche

1. Isoliertes Nucleinsäuremolekül, umfassend eine Nucleotidsequenz, die für ein Polypeptid mit zumindest 90 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) kodiert.

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2. Isoliertes Nucleinsäuremolekül nach Anspruch 1, worin das kodierte Polypeptid zumindest 95 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) aufweist.
- 5 3. Isoliertes Nucleinsäuremolekül nach Anspruch 2, worin das kodierte Polypeptid zumindest 98 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) aufweist.
4. Isoliertes Nucleinsäuremolekül nach Anspruch 3, worin das kodierte Polypeptid zumindest 99 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) aufweist.
- 10 5. Isoliertes Nucleinsäuremolekül nach Anspruch 4, worin das kodierte Polypeptid die Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) aufweist.
6. Isoliertes Nucleinsäuremolekül nach Anspruch 5, das die Kodierregion von Seq.-ID Nr. 3 umfasst.
- 15 7. Isoliertes Nucleinsäuremolekül nach Anspruch 1, das die Fibrinogen-ähnliche Domäne von Seq.-ID Nr. 3 umfasst.
8. Vektor, der ein Nucleinsäuremolekül nach einem der Ansprüche 1 bis 7 umfasst.
9. Rekombinante Wirtszelle, die mit einem Nucleinsäuremolekül nach einem der Ansprüche 1 bis 7 transformiert ist.
- 20 10. Rekombinante Wirtszelle nach Anspruch 9, die eine prokaryotische Zelle ist.
11. Rekombinante Wirtszelle nach Anspruch 9, die eine eukaryotische Zelle ist.
- 25 12. Isoliertes Polypeptid, umfassend eine NL3-Aminosäuresequenz mit zumindest 90 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4).
13. Isoliertes Polypeptid nach Anspruch 12, umfassend eine NL3-Aminosäuresequenz mit zumindest 95 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4).
- 30 14. Isoliertes Polypeptid nach Anspruch 13, umfassend eine NL3-Aminosäuresequenz mit zumindest 98 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4).
15. Isoliertes Polypeptid nach Anspruch 14, umfassend eine NL3-Aminosäuresequenz mit zumindest 99 % Sequenzidentität mit der Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4).
- 35 16. Isoliertes Polypeptid nach Anspruch 15, umfassend eine NL3-Aminosäuresequenz, die die Aminosäuresequenz von nativem menschlichem NL3-Polypeptid (Seq.-ID Nr. 4) aufweist.
- 40 17. Antikörper, der sich spezifisch an die NL3-Aminosäuresequenz des Polypeptids nach einem der Ansprüche 12 bis 16 bindet.
18. Antikörper nach Anspruch 17, der ein monoklonaler Antikörper ist.
- 45 19. Antikörper nach Anspruch 18, der Reste von nicht-menschlicher komplementaritätsbestimmender Region (CDR) und Reste von menschlichem Gerüst (FR) aufweist.
20. Antikörper nach Anspruch 17, der markiert ist.
- 50 21. Zusammensetzung, umfassend ein Polypeptid nach einem der Ansprüche 12 bis 16 in Verbindung mit einem Träger.
22. Zusammensetzung, umfassend einen Antikörper nach Anspruch 17 in Verbindung mit einem Träger.
23. Zusammensetzung nach Anspruch 22, weiters umfassend einen zweiten Antikörper oder ein zytotoxisches oder chemotherapeutisches Mittel.
- 55 24. Konjugat, umfassend ein Polypeptid nach einem der Ansprüche 12 bis 16 oder einen Antikörper nach Anspruch 17, fusioniert an ein weiteres therapeutisches oder zytotoxisches Mittel.

25. Konjugat nach Anspruch 24, worin das weitere therapeutische Mittel ein Toxin, ein unterschiedlicher TIE-Ligand oder ein Mitglied der Gefäßendothelwachstumsfaktor- (VEGF-) Familie ist.
26. Polypeptid nach einem der Ansprüche 12 bis 16 oder Antikörper nach Anspruch 17 zur Verwendung in einem medizinischen Behandlungsverfahren.
27. Verwendung eines Polypeptids nach einem der Ansprüche 12 bis 16 bei der Herstellung eines Medikaments zur Induktion von Endothelzellenapoptose oder Inhibierung von Tumorwachstum.

Revendications

1. Molécule d'acide nucléique isolée comprenant une séquence de nucléotides codant pour un polypeptide ayant une identité de séquence d'au moins 90 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
2. Molécule d'acide nucléique isolée suivant la revendication 1, dans laquelle le polypeptide codé a une identité de séquence d'au moins 95 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
3. Molécule d'acide nucléique isolée suivant la revendication 2, dans laquelle le polypeptide codé a une identité de séquence d'au moins 98 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
4. Molécule d'acide nucléique isolée suivant la revendication 3, dans laquelle le polypeptide codé a une identité de séquence d'au moins 99 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
5. Molécule d'acide nucléique isolée suivant la revendication 4, dans laquelle le polypeptide codé a la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
6. Molécule d'acide nucléique isolée suivant la revendication 5, qui comprend la région codante de la SEQ ID N° 3.
7. Molécule d'acide nucléique isolée suivant la revendication 1, qui comprend le domaine de type fibrinogène de la SEQ ID N° 3.
8. Vecteur qui comprend une molécule d'acide nucléique de l'une quelconque des revendications 1 à 7.
9. Cellule hôte recombinante transformée avec une molécule d'acide nucléique de l'une quelconque des revendications 1 à 7.
10. Cellule hôte recombinante suivant la revendication 9, qui est une cellule procaryotique.
11. Cellule hôte recombinante suivant la revendication 9, qui est une cellule eucaryotique.
12. Polypeptide isolé, comprenant une séquence d'acides aminés de NL3 ayant une identité de séquence d'au moins 90 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
13. Polypeptide isolé suivant la revendication 12, comprenant une séquence d'acides aminés de NL3 ayant une identité de séquence d'au moins 95 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
14. Polypeptide isolé suivant la revendication 13, comprenant une séquence d'acides aminés de NL3 ayant une identité de séquence d'au moins 98 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
15. Polypeptide isolé suivant la revendication 14, comprenant une séquence d'acides aminés de NL3 ayant une identité de séquence d'au moins 99 % avec la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
16. Polypeptide isolé suivant la revendication 15, comprenant une séquence d'acides aminés de NL3 ayant la séquence d'acides aminés du polypeptide NL3 humain naturel (SEQ ID N° 4).
17. Anticorps qui se lie spécifiquement à la séquence d'acides aminés de NL3 du polypeptide suivant l'une quelconque

des revendications 12 à 16.

18. Anticorps suivant la revendication 17, qui est un anticorps monoclonal.

5 **19.** Anticorps suivant la revendication 18, qui possède des résidus de région de détermination de complémentarité (CDR) non humains et des résidus d'ossature (FR) humains.

20. Anticorps suivant la revendication 17 qui est marqué.

10 **21.** Composition comprenant un polypeptide de l'une quelconque des revendications 12 à 16 en association avec un support.

22. Composition comprenant un anticorps de la revendication 17 en association avec un support.

15 **23.** Composition de la revendication 22, comprenant en outre un second anticorps ou un agent cytotoxique ou chimiothérapeutique.

24. Conjugué comprenant un polypeptide de l'une quelconque des revendications 12 à 16 ou un anticorps de la revendication 17, fusionné à un agent thérapeutique ou cytotoxique supplémentaire.

20 **25.** Conjugué suivant la revendication 24, dans lequel l'agent thérapeutique supplémentaire est une toxine, un ligand TIE différent ou un membre de la famille du facteur de croissance endothéliale vasculaire (VEGF).

25 **26.** Polypeptide suivant l'une quelconque des revendications 12 à 16, ou anticorps suivant la revendication 17, destiné à être utilisé dans une méthode de traitement médical.

27. Utilisation d'un polypeptide suivant l'une quelconque des revendications 12 à 16 dans la préparation d'un médicament destiné à l'induction de l'apoptose des cellules endothéliales ou à l'inhibition de la croissance tumorale.

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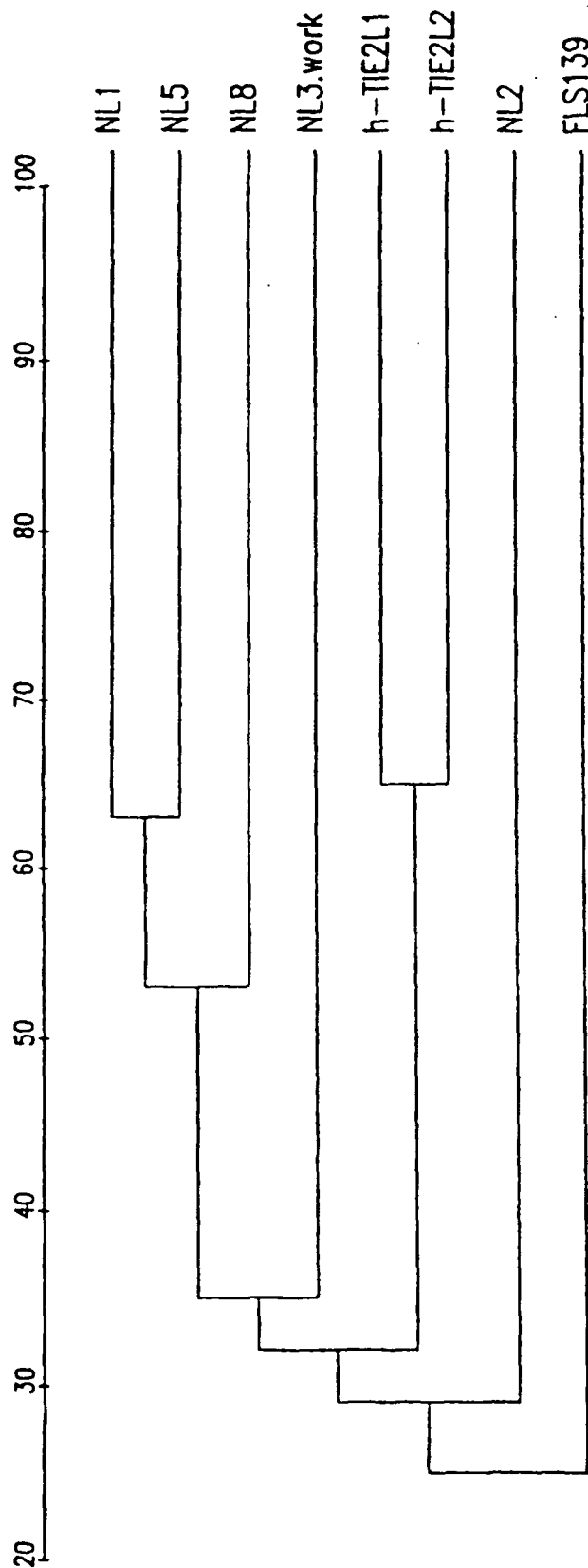


FIG. 1

SEQ ID NO:1:

GCCGAGCTGA GCGGATCCTC ACATGACTGT GATCCGATTC TTTCCAGCGG 50
 CTTCTGCAAC CAAGCGGGTC TTACCCCCGG TCCTCCGCGT CTCCAGTCCT 100
 CGCACCTGGA ACCCCAACGT CCCCAGAGAGT CCCCGAATCC CCGCTCCCAG 150
 GCTACCTAAG AGGATGAGCG GTGCTCCGAC GGCCGGGGCA GCCCTGATGC 200
 TCTGCGCCGC CACCGCCGTG CTACTGAGCG CTCAGGGCGG ACCCGTGCAG 250
 TCCAAGTCGC CGCGCTTTGC GTCCTGGGAC GAGATGAATG TCCTGGCGCA 300
 CGGACTCCTG CAGCTCGGCC AGGGGCTGCG CGAACACGCG GAGCGCACCC 350
 GCAGTCAGCT GAGCGCGCTG GAGCGGCGCC TGAGCGCGTG CGGGTCCGCC 400
 TGTCAGGGAA CCGAGGGGTC CACCGACCTC CCGTTAGCCC CTGAGAGCCG 450
 GGTGGACCCT GAGGTCCTTC ACAGCCTGCA GACACAACTC AAGGCTCAGA 500
 ACAGCAGGAT CCAGCAACTC TTCCACAAGG TGGCCCAGCA GCAGCGGCAC 550
 CTGGAGAAGC AGCACCTGCG AATTCAGCAT CTGCAAAGCC AGTTTGGCCT 600
 CCTGGACCAC AAGCACCTAG ACCATGAGGT GGCCAAGCCT GCCCGAAGAA 650
 AGAGGCTGCC CGAGATGGCC CAGCCAGTTG ACCCGGCTCA CAATGTCAGC 700
 CGCCTGCACC GGCTGCCCAG GGATTGCCAG GAGCTGTTC AGGTTGGGGA 750
 GAGGCAGAGT GGA CTATTTG AAATCCAGCC TCAGGGGTCT CCGCCATTTT 800
 TGGTGA ACTG CAAGATGACC TCAGATGGAG GCTGGACAGT AATTCAGAGG 850
 CGCCACGATG GCTCAGTGGA CTTCAACCGG CCCTGGGAAG CCTACAAGGC 900
 GGGGTTTGGG GATCCCCACG GCGAGTTCTG GCTGGGTCTG GAGAAGGTGC 950
 ATAGCATCAC GGGGGACCGC AACAGCCGCC TGGCCGTGCA GCTGCGGGAC 1000
 TGGGATGGCA ACGCCGAGTT GCTGCAGTTC TCCGTGCACC TGGGTGGCGA 1050
 GGACACGGCC TATAGCCTGC AGCTCACTGC ACCCGTGGCC GGCCAGCTGG 1100
 GCGCCACCAC CGTCCCACCC AGCGGCCTCT CCGTACCCTT CTCCACTTGG 1150

FIG. 2A

GACCAGGATC ACGACCTCCG CAGGGACAAG AACTGCGCCA AGAGCCTCTC 1200
 TGGAGGCTGG TGGTTTGGA CCTGCAGCCA TTCCAACCTC AACGGCCAGT 1250
 ACTTCCGCTC CATCCCACAG CAGCGGCAGA AGCTTAAGAA GGGAATCTTC 1300
 TGGAAGACCT GCGGGGGCCG CTACTACCCG CTGCAGGCCA CCACCATGTT 1350
 GATCCAGCCC ATGGCAGCAG AGGCAGCCTC CTAGCGTCCT GGCTGGGCCT 1400
 GGTCCCAGGC CCACGAAAGA CGGTGACTCT TGGCTCTGCC CGAGGATGTG 1450
 GCCGTTCCCT GCCTGGGCAG GGGCTCCAAG GAGGGGCCAT CTGGAAGCTT 1500
 GTGGACAGAG AAGAAGACCA CGACTGGAGA AGCCCCCTTT CTGAGTGCAG 1550
 GGGGGCTGCA TCGTTGCCT CCTGAGATCG AGGCTGCAGG ATATGCTCAG 1600
 ACTCTAGAGG CGTGGACCAA GGGGCATGGA GCTTCACTCC TTGCTGGCCA 1650
 GGGAGTTGGG GACTCAGAGG GACCACTTGG GGCCAGCCAG ACTGGCCTCA 1700
 ATGGCGGACT CAGTCACATT GACTGACGGG GACCAGGGCT TGTGTGGGTC 1750
 GAGAGCGCCC TCATGGTGCT GGTGCTGTTG TGTGTAGGTC CCCTGGGGAC 1800
 ACAAGCAGGC GCCAATGGTA TCTGGGCGGA GCTCACAGAG TTCTTGGAAT 1850
 AAAAGCAACC TCAGAACAC 1869

FIG. 2B

SEQ ID NO:2:

Met	Ser	Gly	Ala	Pro	Thr	Ala	Gly	Ala	Ala	Leu	Met	Leu	Cys	Ala	1	5	10	15
Ala	Thr	Ala	Val	Leu	Leu	Ser	Ala	Gln	Gly	Gly	Pro	Val	Gln	Ser	20	25	30	
Lys	Ser	Pro	Arg	Phe	Ala	Ser	Trp	Asp	Glu	Met	Asn	Val	Leu	Ala	35	40	45	
His	Gly	Leu	Leu	Gln	Leu	Gly	Gln	Gly	Leu	Arg	Glu	His	Ala	Glu	50	55	60	
Arg	Thr	Arg	Ser	Gln	Leu	Ser	Ala	Leu	Glu	Arg	Arg	Leu	Ser	Ala	65	70	75	
Cys	Gly	Ser	Ala	Cys	Gln	Gly	Thr	Glu	Gly	Ser	Thr	Asp	Leu	Pro	80	85	90	
Leu	Ala	Pro	Glu	Ser	Arg	Val	Asp	Pro	Glu	Val	Leu	His	Ser	Leu	95	100	105	
Gln	Thr	Gln	Leu	Lys	Ala	Gln	Asn	Ser	Arg	Ile	Gln	Gln	Leu	Phe	110	115	120	
His	Lys	Val	Ala	Gln	Gln	Gln	Arg	His	Leu	Glu	Lys	Gln	His	Leu	125	130	135	
Arg	Ile	Gln	His	Leu	Gln	Ser	Gln	Phe	Gly	Leu	Leu	Asp	His	Lys	140	145	150	
His	Leu	Asp	His	Glu	Val	Ala	Lys	Pro	Ala	Arg	Arg	Lys	Arg	Leu	155	160	165	
Pro	Glu	Met	Ala	Gln	Pro	Val	Asp	Pro	Ala	His	Asn	Val	Ser	Arg	170	175	180	
Leu	His	Arg	Leu	Pro	Arg	Asp	Cys	Gln	Glu	Leu	Phe	Gln	Val	Gly	185	190	195	
Glu	Arg	Gln	Ser	Gly	Leu	Phe	Glu	Ile	Gln	Pro	Gln	Gly	Ser	Pro	200	205	210	
Pro	Phe	Leu	Val	Asn	Cys	Lys	Met	Thr	Ser	Xaa	Gly	Gly	Trp	Thr	215	220	225	
Val	Ile	Gln	Arg	Arg	His	Asp	Gly	Ser	Val	Asp	Phe	Asn	Arg	Pro	230	235	240	

FIG. 3A

Trp	Glu	Ala	Tyr	Lys	Ala	Gly	Phe	Gly	Asp	Pro	His	Gly	Glu	Phe
				245					250					255
Trp	Leu	Gly	Leu	Glu	Lys	Val	His	Ser	Ile	Thr	Gly	Asp	Arg	Asn
				260					265					270
Ser	Arg	Leu	Ala	Val	Gln	Leu	Arg	Asp	Trp	Asp	Gly	Asn	Ala	Glu
				275					280					285
Leu	Leu	Gln	Phe	Ser	Val	His	Leu	Gly	Gly	Glu	Asp	Thr	Ala	Tyr
				290					295					300
Ser	Leu	Gln	Leu	Thr	Ala	Pro	Val	Ala	Gly	Gln	Leu	Gly	Ala	Thr
				305					310					315
Thr	Val	Pro	Pro	Ser	Gly	Leu	Ser	Val	Pro	Phe	Ser	Thr	Trp	Asp
				320					325					330
Gln	Asp	His	Asn	Leu	Arg	Arg	Asp	Lys	Asn	Cys	Ala	Lys	Ser	Leu
				335					340					345
Ser	Gly	Gly	Trp	Trp	Phe	Gly	Thr	Cys	Ser	His	Ser	Asn	Leu	Asn
				350					355					360
Gly	Gln	Tyr	Phe	Arg	Ser	Ile	Pro	Gln	Gln	Arg	Gln	Lys	Leu	Lys
				365					370					375
Lys	Gly	Ile	Phe	Trp	Lys	Thr	Trp	Arg	Gly	Arg	Tyr	Tyr	Pro	Leu
				380					385					390
Gln	Ala	Thr	Thr	Met	Leu	Ile	Gln	Pro	Met	Ala	Ala	Glu	Ala	Ala
				395					400					405
Ser														
406														

FIG. 3B

SEQ ID NO:3:

CGGACGCGTG GGGCCCTGGT GGGCCCAGCA AGATGGATCT ACTGTGGATC 50
 CTGCCCTCCC TGTGGCTTCT CCTGCTTGGG GGGCCTGCCT GCCTGAAGAC 100
 CCAGGAACAC CCCAGCTGCC CAGGACCCAG GGAAGTGGAA GCCAGCAAAG 150
 TTGTCCTCCT GCCCAGTTGT CCCGGAGCTC CAGGAAGTCC TGGGGAGAAG 200
 GGAGCCCCAG GTCCTCAAGG GCCACCTGGA CCACCAGGCA AGATGGGCCC 250
 CAAGGGTGAG CCAGGCCCCA' GAAACTGCCG GGAGCTGTTG AGCCAGGGCG 300
 CCACCTTGAG CGGCTGGTAC CATCTGTGCC TACCTGAGGG CAGGGCCCTC 350
 CCAGTCTTTT GTGACATGGA CACCGAGGGG GCGGCTGGC TGGTGTTC 400
 GAGGCGCCAG GATGGTTCTG TGGATTTCTT CCGCTCTTGG TCCTCCTACA 450
 GAGCAGGTTT TGGGAACCAA GAGTCTGAAT TCTGGCTGGG AAATGAGAAT 500
 TTGCACCAGC TTA CTCTCCA GGGTAACTGG GAGCTGCGGG TAGAGCTGGA 550
 AGACTTTAAT GGTAACCGTA CTTTCGCCCA CTATGCGACC TTCCGCCTCC 600
 TCGGTGAGGT AGACCACTAC CAGCTGGCAC TGGGCAAGTT CTCAGAGGGC 650
 ACTGCAGGGG ATTCCCTGAG CCTCCACAGT GGGAGGCCCT TTACCACCTA 700
 TGACGCTGAC CACGATTCAA GCAACAGCAA CTGTGCAGTG ATTGTCCACG 750
 GTGCCTGGTG GTATGCATCC TGTTACCGAT CAAATCTCAA TGGTCGCTAT 800
 GCAGTGTCTG AGGCTGCCGC CCACAAATAT GGCATTGACT GGGCCTCAGG 850
 CCGTGGTGTG GGCCACCCCT ACCGCAGGGT TCGGATGATG CTTGATAGG 900
 GCACTCTGGC AGCCAGTGCC CTTATCTCTC CTGTACAGCT TCCGGATCGT 950
 CAGCCACCTT GCCTTTGCCA ACCACCTCTG CTTGCCTGTC CACATTTAAA 1000
 AATAAAATCA TTTTAGCCCT TTCA 1024

FIG. 4

SEQ ID NO:4:

Met	Asp	Leu	Leu	Trp	Ile	Leu	Pro	Ser	Leu	Trp	Leu	Leu	Leu	Leu		1	5	10	15
Gly	Gly	Pro	Ala	Cys	Leu	Lys	Thr	Gln	Glu	His	Pro	Ser	Cys	Pro		20	25	30	
Gly	Pro	Arg	Glu	Leu	Glu	Ala	Ser	Lys	Val	Val	Leu	Leu	Pro	Ser		35	40	45	
Cys	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Gly	Glu	Lys	Gly	Ala	Pro	Gly		50	55	60	
Pro	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Lys	Met	Gly	Pro	Lys	Gly		65	70	75	
Glu	Pro	Gly	Pro	Arg	Asn	Cys	Arg	Glu	Leu	Leu	Ser	Gln	Gly	Ala		80	85	90	
Thr	Leu	Ser	Gly	Trp	Tyr	His	Leu	Cys	Leu	Pro	Glu	Gly	Arg	Ala		95	100	105	
Leu	Pro	Val	Phe	Cys	Asp	Met	Asp	Thr	Glu	Gly	Gly	Gly	Trp	Leu		110	115	120	
Val	Phe	Gln	Arg	Arg	Gln	Asp	Gly	Ser	Val	Asp	Phe	Phe	Arg	Ser		125	130	135	
Trp	Ser	Ser	Tyr	Arg	Ala	Gly	Phe	Gly	Asn	Gln	Glu	Ser	Glu	Phe		140	145	150	
Trp	Leu	Gly	Asn	Glu	Asn	Leu	His	Gln	Leu	Thr	Leu	Gln	Gly	Asn		155	160	165	
Trp	Glu	Leu	Arg	Val	Glu	Leu	Glu	Asp	Phe	Asn	Gly	Asn	Arg	Thr		170	175	180	
Phe	Ala	His	Tyr	Ala	Thr	Phe	Arg	Leu	Leu	Gly	Glu	Val	Asp	His		185	190	195	
Tyr	Gln	Leu	Ala	Leu	Gly	Lys	Phe	Ser	Glu	Gly	Thr	Ala	Gly	Asp		200	205	210	
Ser	Leu	Ser	Leu	His	Ser	Gly	Arg	Pro	Phe	Thr	Thr	Tyr	Asp	Ala		215	220	225	
Asp	His	Asp	Ser	Ser	Asn	Ser	Asn	Cys	Ala	Val	Ile	Val	His	Gly		230	235	240	
Ala	Trp	Trp	Tyr	Ala	Ser	Cys	Tyr	Arg	Ser	Asn	Leu	Asn	Gly	Arg		245	250	255	
Tyr	Ala	Val	Ser	Glu	Ala	Ala	Ala	His	Lys	Tyr	Gly	Ile	Asp	Trp		260	265	270	
Ala	Ser	Gly	Arg	Gly	Val	Gly	His	Pro	Tyr	Arg	Arg	Val	Arg	Met		275	280	285	
Met	Leu	Arg														288			

FIG. 5

SEQ ID NO:5:

GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
 GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
 ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150
 ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
 TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
 TTCAAAAACCT CAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
 ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
 ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
 CAAAACCTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
 AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
 TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
 ATAATAGCAT CAAAGACCTT CTCCAGACCG TGAAGACCA ATATAACAA 600
 TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
 GACTAGTATT CAAGAACCCA CAGAAATTC TCTATCTTCC AAGCCAAGAG 700
 CACCAAGAAC TACTCCCTTT CTTCACTTGA ATGAAATAAG AAATGTAAAA 750
 CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
 TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTTCATG 850
 TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
 ATAGATGGAT CACAAAACCT CAATGAAACG TGGGAGAACT ACAAATATGG 950
 TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
 CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050
 AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100
 AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150

FIG. 6A

CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200
 AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250
 TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300
 CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGA GTCTCAAAAT 1350
 GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400
 TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450
 TAACTCATTG CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500
 AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550
 AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600
 AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650
 CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700
 AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750
 ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAAACTA GTACTCTTGT 1800
 TAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850
 TAAATGTTGT AGTATTAATT TCAAACTAA AAATCGTCAG CACAGAGTAT 1900
 GTGTAAAAAT CTGTAATACA AATTTTTTAAA CTGATGCTTC ATTTTGCTAC 1950
 AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000
 AAGCAGAATT AAATACTGTA TTAAATAAG TTCGCTGTCT TT 2042

FIG. 6B

SEQ ID NO:6:

Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile	1	5	10	15
Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser	20	25	30	
Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile	35	40	45	
Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe	50	55	60	
Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu	65	70	75	
Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser	80	85	90	
Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys	95	100	105	
Leu	Gln	Val	Lys	Asn	Glu	Glu	Val	Lys	Asn	Met	Ser	Leu	Glu	Leu	110	115	120	
Asn	Ser	Lys	Leu	Glu	Ser	Leu	Leu	Glu	Glu	Lys	Ile	Leu	Leu	Gln	125	130	135	
Gln	Lys	Val	Lys	Tyr	Leu	Glu	Glu	Gln	Leu	Thr	Asn	Leu	Ile	Gln	140	145	150	
Asn	Gln	Pro	Glu	Thr	Pro	Glu	His	Pro	Glu	Val	Thr	Ser	Leu	Lys	155	160	165	
Thr	Phe	Val	Glu	Lys	Gln	Asp	Asn	Ser	Ile	Lys	Asp	Leu	Leu	Gln	170	175	180	
Thr	Val	Glu	Asp	Gln	Tyr	Lys	Gln	Leu	Asn	Gln	Gln	His	Ser	Gln	185	190	195	
Ile	Lys	Glu	Ile	Glu	Asn	Gln	Leu	Arg	Arg	Thr	Ser	Ile	Gln	Glu	200	205	210	
Pro	Thr	Glu	Ile	Ser	Leu	Ser	Ser	Lys	Pro	Arg	Ala	Pro	Arg	Thr	215	220	225	
Thr	Pro	Phe	Leu	Gln	Leu	Asn	Glu	Ile	Arg	Asn	Val	Lys	His	Asp	230	235	240	

FIG. 7A

Gly	Ile	Pro	Ala	Glu	Cys	Thr	Thr	Ile	Tyr	Asn	Arg	Gly	Glu	His
				245					250					255
Thr	Ser	Gly	Met	Tyr	Ala	Ile	Arg	Pro	Ser	Asn	Ser	Gln	Val	Phe
				260					265					270
His	Val	Tyr	Cys	Asp	Val	Ile	Ser	Gly	Ser	Pro	Trp	Thr	Leu	Ile
				275					280					285
Gln	His	Arg	Ile	Asp	Gly	Ser	Gln	Asn	Phe	Asn	Glu	Thr	Trp	Glu
				290					295					300
Asn	Tyr	Lys	Tyr	Gly	Phe	Gly	Arg	Leu	Asp	Gly	Glu	Phe	Trp	Leu
				305					310					315
Gly	Leu	Glu	Lys	Ile	Tyr	Ser	Ile	Val	Lys	Gln	Ser	Asn	Tyr	Val
				320					325					330
Leu	Arg	Ile	Glu	Leu	Glu	Asp	Trp	Lys	Asp	Asn	Lys	His	Tyr	Ile
				335					340					345
Glu	Tyr	Ser	Phe	Tyr	Leu	Gly	Asn	His	Glu	Thr	Asn	Tyr	Thr	Leu
				350					355					360
His	Leu	Val	Ala	Ile	Thr	Gly	Asn	Val	Pro	Asn	Ala	Ile	Pro	Glu
				365					370					375
Asn	Lys	Asp	Leu	Val	Phe	Ser	Thr	Trp	Asp	His	Lys	Ala	Lys	Gly
				380					385					390
His	Phe	Asn	Cys	Pro	Glu	Gly	Tyr	Ser	Gly	Gly	Trp	Trp	Trp	His
				395					400					405
Asp	Glu	Cys	Gly	Glu	Asn	Asn	Leu	Asn	Gly	Lys	Tyr	Asn	Lys	Pro
				410					415					420
Arg	Ala	Lys	Ser	Lys	Pro	Glu	Arg	Arg	Arg	Gly	Leu	Ser	Trp	Lys
				425					430					435
Ser	Gln	Asn	Gly	Arg	Leu	Tyr	Ser	Ile	Lys	Ser	Thr	Lys	Met	Leu
				440					445					450
Ile	His	Pro	Thr	Asp	Ser	Glu	Ser	Phe	Glu					
				455					460					

FIG. 7B

NL3 Northern

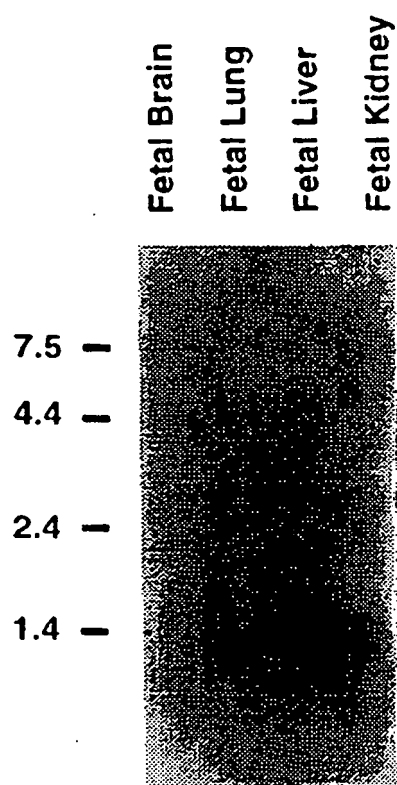


FIG. 9